



#3

## Sequence Listing

- <110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.
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                     155                    160                    165  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala  
                     170                    175                    180  
 Gly Leu Ala Leu Glu Ile Arg Ser Leu  
                     185

<110> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

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 ttctgtggac togtaaagga aaactaaaga ttgaagacat cactgataag 200  
 tacattttta tcaactggatg tgaactgggc tttgaaaact tggcagccag 250  
 aacttttgat aaaaagggat ttcatgtaat cgctgcctgt ctgactgaat 300  
 caggatcaac agcttttaaag gcagaaaact cagagagact togtactgtg 350  
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400  
 gaagaaccaa gttggggaga aaggctctctg gggctctgac aataatgctg 450  
 gtgttcccg cgctgtggct cccactgact ggttgacact agaggactac 500  
 agagaacctt ttgaagtga cctgttttga ctcatcagtg tgacaactaa 550  
 tatgcttctt ttggtcaaga aagctcaagg gagagtatt aatgtctcca 600  
 gtgttggagg togccttgca atcgttggag ggggtatac tccatccaaa 650  
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 tggtytgac gtctcatgca ttgaaccagg attgttcaaa aaaaacttgg 750  
 cagatccagt aaaggtaatt gaaaaaaaaa togcatttg ggagcagctg 800  
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 tatgcgctg gaaaagatgc caaaattttt tggatacctc tgtctccat 1000  
 gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050  
 ctaatcccaa ggcagtgtga ctcagctaac caccaatgtc toctccagc 1100  
 tatgaaattg gcgatttca agaacacatc tctttttcaa cccattct 1150  
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 agggagtccc accatcgctg gtggtatccc agggctcctg ctcaagtttt 1250  
 ctttgaaaag gagggctgga atggtacac acataggcaa gtctgccc 1300  
 gtatttaagg tttgcctgct tgggtgtgat taagggaat tgaaagaatt 1350  
 gccattcaa aatgatcttt accgtggcct gcccatgct tatggctccc 1400  
 agcatttaca gtaacttgtg aatgttaagt atcatctctt atctaaatat 1450  
 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 36-47, 108-113, 166-171, 198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

<400> 10  
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu  
1 5 10 15  
  
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120



Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val					

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

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 ggccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgc 150  
 gccgcctcat cgggaattca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa ctgggtgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 ggggttaaac cagcaaatec acccgtctta ccagctcctc agaaggcgga 450  
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 ctgaaggatg ggaccacgga ggaggccaca aaaaggcaag aagccccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcctc agctggaggg 650  
 gagcggatg cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
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 agtgcctctg aactatcgcc agaaggcggt gattgacgtc ttctgcatg 800  
 catggaaagg ataccgcaag ttgcatggg gccatgacga gctgaagcct 850  
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
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 aacctgtttg agagcacgat ccgcctcctg ggggggctcc tgagtgccta 1050  
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cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
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 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100  
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 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
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 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

1	5	10	15
Gln Ser Asp Phe	Leu Thr Pro Pro	Val Gly Gly Ala	Pro Trp Ala
	20	25	30
Val Ala Thr Thr	Val Val Met Tyr	Pro Pro Pro Pro	Pro Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr	Leu Ser Phe Gly	Glu Ser Tyr
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg	Arg Ser Cys Trp	Arg Lys Trp
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg	Asn Met Ile Leu	Phe Leu Leu
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu	Leu Phe Tyr Ile	Asn Leu Ala
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe	Arg Leu Glu Glu	Glu Gln Lys
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu	Lys Pro Ala Asn	Pro Pro Val
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp	Thr Asp Pro Glu	Asn Leu Pro
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln	Arg His Ile Gln	Arg Gly Pro
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro	Ser Gln Asp Leu	Lys Asp Gly
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg	Gln Glu Ala Pro	Val Asp Pro
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg	Thr Val Ile Ser	Trp Arg Gly
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly	Thr Glu Leu Pro	Ser Arg Arg
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro	Leu Pro Pro Ala	Arg Thr Gln
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr	Arg Gln Lys Gly	Val Ile Asp
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly	Tyr Arg Lys Phe	Ala Trp Gly
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser	Arg Ser Phe Ser	Glu Trp Phe
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp	Ala Leu Asp Thr	Met Trp Ile

290	295	300
Leu Gly Leu Arg Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser
305	310	315
Lys Lys Leu His Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu
320	325	330
Ser Thr Ile Arg Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu
335	340	345
Ser Gly Asp Ser Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn
350	355	360
Arg Leu Met Pro Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser
365	370	375
Asp Val Asn Ile Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr
380	385	390
Ser Asp Ser Thr Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe
395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala
410	415	420
Val Glu Lys Val Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val

	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala
	680	685	690
His Pro Leu Pro	Ile Trp Thr Pro Ala		
	695		

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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cccatgcgcc gccgcctctc cgacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggctc gggttgctct ccggcggcct 150  
ccctcggaag tgttcctct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250  
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ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcagtgtg gtgcccttc gcgaacgctt cgaggagctc 400  
ctgggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgtca accaggtgga ccacttcagg ttcaaccggg 500  
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attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
tggtcttctc gaggtgggc ccttcacgt ggcctccccg gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcctctgct gctctccaag 700  
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
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ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
acaggagcag ttcaaggtg acagggagg aggcctgaac actgtgaagt 950  
accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgact 1000  
gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> FRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
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 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
 20 25 30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
 35 40 45



Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
 50 55 60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
 65 70 75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
 80 85 90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
 95 100 105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
 110 115 120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
 125 130 135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu  
 140 145 150  
 Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp  
 155 160 165  
 Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala  
 170 175 180  
 Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His  
 185 190 195  
 Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His  
 200 205 210  
 Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly  
 215 220 225  
 Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu  
 230 235 240  
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe  
 245 250 255  
 Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg  
 260 265 270  
 Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly  
 275 280 285  
 Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu  
 290 295 300  
 Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp  
 305 310 315  
 Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser  
 320 325

<210> 18  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
gcgaacgctt cgaggagtc tgg 23

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
gcagtgccggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
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<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gactggctgg tgcccagaaa gtctctttctg ccactgacgc ccccatcagg 150  
gattggggcct tctttccccc ttctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag ccagccccc tggggaaggg gagaaagtgg 250  
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ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc\_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggccccc gccgcgctcc tgcccgcccg 150

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<212> PRT  
<213> Homo sapiens

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<222> 1-33  
<223> Signal peptide.

<220>  
<221> TRANSMEM  
<222> 13-40  
<223> Transmembrane domain (type II).

<400> 24

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Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	50	55	60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	65	70	75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	80	85	90	
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Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	245	250	255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	275	280	285	

Thr Asp Glu Ser	Gln Gly Ile Phe Val	Glu Lys Asn Met Ile His	290	300
Asn Cys Ser Leu	Ile Ala Ser Ala Leu Thr	Ile Ser Asn Ile Gln	305	315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys His	Val Gln Thr Lys Arg	320	330
Gly Asn Asn Thr	Arg Thr Val Asp Ile Val	Val Leu Glu Ser Ser	335	345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val Val	Asn Asn Lys Gly Asp	350	360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly Ile	Thr Ala Tyr Leu Gln	365	375
Cys Thr Arg Asn	Thr His Gly Ser Gly Ile	Tyr Pro Gly Asn Pro	380	390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg Cys	Asp Arg Gly Gly Phe	395	405
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys Gln	Tyr Ala Asn Asp Val	410	420
Thr Arg Val Leu	Tyr Met Phe Asn Gln Met	Pro Leu Asn Leu Thr	425	435
Asn Ala Val Ala	Thr Ala Arg Gln Leu Leu	Ala Tyr Thr Val Glu	440	450
Ala Ala Asn Phe	Ser Asp Lys Met Asp Val	Ile Phe Val Ala Glu	455	465
Met Ile Glu Lys	Phe Gly Arg Phe Thr Lys	Glu Glu Lys Ser Lys	470	480
Glu Leu Gly Asp	Val Met Val Asp Ile Ala	Ser Asn Ile Met Leu	485	495
Ala Asp Glu Arg	Val Leu Trp Leu Ala Gln	Arg Glu Ala Lys Ala	500	510
Cys Ser Arg Ile	Val Gln Cys Leu Gln Arg	Ile Ala Thr Tyr Arg	515	525
Leu Ala Gly Gly	Ala His Val Tyr Ser Thr	Tyr Ser Pro Asn Ile	530	540
Ala Leu Glu Ala	Tyr Val Ile Lys Ser Thr	Gly Phe Thr Gly Met	545	555
Thr Cys Thr Val	Phe Gln Lys Val Ala Ala	Ser Asp Arg Thr Gly	560	570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys  
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu  
590 595 600

Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr  
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Ser

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

aactggaaaag gaaggctgtc tccc 24

<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

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<210> 18

<211> 683

<212> DNA

<213> Homo sapiens

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150



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 <223> Signal peptide.

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 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
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 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30

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<211> 322  
<212> PRT  
<213> Homo sapiens

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35 40 45  
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
50 55 60  
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
65 70 75  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
80 85 90  
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
95 100 105

Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	110	115	120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	290	295	300
Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala	305	310	315
His Leu Val Phe Val Lys Val	320		

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
 50 55 60  
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
 65 70 75  
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
 80 85 90  
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
 95 100 105  
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
 110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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<210> 35  
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<400> 35  
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<210> 36  
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<213> Artificial Sequence

<220>  
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<400> 36  
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<210> 37  
<211> 23  
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<220>  
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<400> 37  
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<210> 38  
<211> 39  
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<400> 38  
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<210> 39  
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<220>  
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<210> 40  
<211> 2084

<212> DNA  
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<400> 40

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<210> 41  
 <211> 334  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
 50 55 60  
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
 65 70 75  
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
 80 85 90  
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
 95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val	110	115	120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser	125	130	135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr	140	145	150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser	155	160	165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val	170	175	180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser	185	190	195
Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu	200	205	210
Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	215	220	225
Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	230	235	240
Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	245	250	255
Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	260	265	270
His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	275	280	285
Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	290	295	300
Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	305	310	315
Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	320	325	330

Arg Thr Ser Val

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20					25						30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35					40						45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50					55						60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65					70						75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80					85						90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95					100						105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110					115						120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125					130						135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140					145						150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155					160						165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170					175						180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185					190						195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200					205						210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215					220						225

Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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 <223> Synthetic oligonucleotide probe

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<210> 45  
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 <223> Synthetic oligonucleotide probe

<400> 45  
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<210> 46  
 <211> 26  
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<400> 46  
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<210> 47  
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<400> 47  
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<210> 48  
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<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
aaaaaaaaa aaaaaaaga 1969

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0211 > 233  
0212 > PRT  
0213 > Homo sapiens

0400 > 50  
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20 25 30  
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
35 40 45  
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
50 55 60  
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
65 70 75  
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

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Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	
				95					100					105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	
				110					115					120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	
				125					130					135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	
				140					145					150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	
				155					160					165	
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
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<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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<212> PRT

<213> Homo sapiens

<400> 52

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Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
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Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
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Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
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<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

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				185					190					195
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				200					205					210
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				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
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cctcagtgtg cgtgacctgg attccccgtg ggaatgggtg gttcccaatc 2250  
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 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
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<210> 58  
 <211> 1115  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
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 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala  
 20 25 30  
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr  
 35 40 45  
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu  
 50 55 60  
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu  
 65 70 75  
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr  
 80 85 90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln	95	100	105
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala	110	115	120
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln	125	130	135
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys	140	145	150
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val	155	160	165
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met	170	175	180
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu	185	190	195
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val	200	205	210
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr	215	220	225
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile	230	235	240
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser	245	250	255
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser	260	265	270
Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375



Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly		665	670	675
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu		680	685	690
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr		695	700	705
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr		710	715	720
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met		725	730	735
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr		740	745	750
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys		755	760	765
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His		770	775	780
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn		785	790	795
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr		800	805	810
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro		815	820	825
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg		830	835	840
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro		845	850	855
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgtg gagg 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 61  
caccoccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50  
cgctgtctcc tcccaggctc ccggggccga ccccccgcga acatgcagcc 100  
cacgggcccgc gagggttccc gcgcgctcag ccggcgggtat ctgcggcgtc 150  
tctgtctect gctactgctg ctgtgtgtgc ggcagcccggt aacccggcgg 200  
gagaccacgc cggggcgcgc cagagccctc tccacgctgg gctcccccag 250  
cctcttcacc acgcggggtg tcccagcgc cctcactacc ccagggtctc 300  
ctacgcacagg caccoccaaa accctggacc ttcggggtcg cgcgcaggcc 350  
ctgatgggga gtttccact cgtggacggc cacaatgacc tgcccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcacgc atgtgtgct 600  
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 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cccatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<210>  
 <211> unsure  
 <212> 196, 386  
 <213> unknown amino acid

<400> 63  
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg  
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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg  
 20 25 30  
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
 35 40 45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
 50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro	65	70	75
Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser	80	85	90
Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg	95	100	105
Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe	110	115	120
Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val	125	130	135
Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp	140	145	150
Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His	155	160	165
Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala	170	175	180
Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val	185	190	195
Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser	200	205	210
Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys	215	220	225
Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met	230	235	240
Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val	245	250	255
Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala	260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro	275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu	290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly	305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu	320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg	335	340	345

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
	350	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
	365	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
	380	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
	395	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
	410	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
	425	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
	440	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
	455	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
	470	480
Thr Phe Thr Gln Trp Leu Cys		
	485	

<210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 64  
 ccttcacctg cagtacacca tgggc 25

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 65  
 gtcacacaca gctctggcag ctgag 25

<210> 66  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgcctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50

aacacccaca gatccctcta tgaactgcaat gtgagggtgc cggcttttgc 100

ggccacagcaa gcttgataag catgaagctc ttatcttttg tggtgtggt 150

cgggtgtttg ctggtgcacc cagctgaagc caacaagagt tctgaagata 200

tccgggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtgggtgga 300

gcccattgcca gtgcctgggc atgaactgga ggccactgc ctgctgtgag 350

agtgacagga caggagagcg agcaccacca ccataaaggc catcattgtc 400

atctactgtt ccgtggtggg tgcctgtttg ctctacatgg ccttctctgat 450

gctggttgga cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

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ccaacacccat ggtgcccagc ttccaggctg gacaaaagcag ggggctactt 750

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aagaggggatg tggctcttga tctctgttgc cttcttgggt ctttggggtt 900

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ctcaggagtg gatgcgatct gtctctctct gctccactct tgcgccttc 1000

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gttcttttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150



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 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
 ctctgtctgc ggccccctca cctgcacttg aggggtcttg gcagtccctc 1350  
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
 gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450  
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
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 ttttatttct ctca 1564

<210> 68  
 <211> 183  
 <212> PFT  
 <213> Homo sapiens

<400> 68  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
                     20                    25                    30  
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
                     35                    40                    45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
                     50                    55                    60  
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
                     65                    70                    75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
                     80                    85                    90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
                     95                    100                    105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
                     110                    115                    120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
                     125                    130                    135  
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
                     140                    145                    150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
                     155                    160                    165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180

Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

<400> 69  
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<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
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20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45  
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
50 55 60  
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
65 70 75  
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
80 85 90  
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
95 100 105  
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255

Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200  
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 ctgaaaaga 1809

<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

275										280					285				
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln					
				290					295					300					
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn					
				305					310					315					
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr					
				320					325					330					
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg					
				335					340					345					
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp					
				350					355					360					

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 73  
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<210> 74  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
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<210> 75  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
 ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens



<400> 76

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tgcactcagc ggtggaggag acggacgcgg ggetgtacac ctgcaacctg 150  
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 caataagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
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 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
 35 40 45  
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
 50 55 60  
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
 65 70 75  
 Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
 80 85 90  
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
 95 100 105  
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
 110 115 120  
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
 125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cgcaccttg cctgcagagg cccgaggacc gttctgtgg cacatacatc 200

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430				435	
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

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<220>  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 81  
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<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 82  
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<210> 83  
 <211> 1844  
 <212> DNA  
 <213> Homo sapiens

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
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taacaggatc gggggccgca ttttcacctc ccgggaccag aacacgggct 400  
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450  
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500  
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
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<210> 84  
 <211> 567  
 <212> FRT  
 <213> Homo sapiens

<400> 84  
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165  
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195

Ala Leu Gly Cys Arg Lys Ala Met Lys	Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu Gly Asp Val Met Ser	Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala Glu Ala Leu Arg Ala	His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala Met Thr Gln Gly Pro	His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro Pro Leu Pro Arg His	Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr Val Pro Ala Thr Lys	Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp Arg Glu Glu His Ile	Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala Ala Leu His Gly Pro	Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly Val Val Lys Arg Trp	Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe Val Val Gln Pro Pro	Ala Leu Trp Gln Thr Glu	455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly	470	475	480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
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<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25				30	

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile		
50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys		
65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg		
80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val		
95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn		
110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu		
125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu		
140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys		
155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His		
170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala		
185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr		
200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu		
215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile		
230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu		
245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro		
260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu		
275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe		
290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys		
305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr		

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	

605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val	Leu Gln Ile Phe Val	His
620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val	Gly Val Val Val Pro	Asp
635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys	Gly
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln	Val Val Arg Glu Ala	Ile
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys	Thr
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu	His Pro Glu Pro Phe	Ser
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg	Gly
710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr	Glu
725	730	735

His Ile Gln Asp

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe		395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr		410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu		425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly		440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys		455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg		470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val		485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly		500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val		515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala		530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu		545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr		560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp		575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp		590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe		605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro		620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu		635	640	645
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<400> 94

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 <212> PRT  
 <213> Homo sapiens

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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
 35 40 45  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
 50 55 60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
 65 70 75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
 80 85 90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
 95 100 105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
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 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
 140 145 150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
 155 160 165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
 170 175 180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
 185 190 195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
 200 205 210



Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	230	235	240
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	245	250	255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	260	265	270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	275	280	285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	290	295	300
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<211> 25

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 97

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 97

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<210> 98

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 99

<211> 1429

<212> DNA  
<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu	Pro Gln Arg Asp Arg Leu	
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	
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Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
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Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
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Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
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Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
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 <212> DNA  
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<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
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Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
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				245					250					255	
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
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His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
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Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
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Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
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Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
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Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
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Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
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Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
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Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
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Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	
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Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	
				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
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Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
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Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
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Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
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Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
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His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
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Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
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Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
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Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
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Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
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Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
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Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
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Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
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Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
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Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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<E10> 104

<E11> 442

<E12> PRT

<E13> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30

Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45

Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60

Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75

Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgetgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108  
ctctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<200>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttcctgtgt ctctgggtgt ttgcctaaac ctgcaaacad 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacggctg ggccggacgc tgggcccgcg cgtgggtctc tgcggggaga 50

cgcacgcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150

gtcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgt ggggtggctc ggccgcccac tgcttcagcc 300

acagagacct ccgcactggc ctgggtggtgc tgggcgcca cgtcctgagt 350

actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400

ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500

gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctg 550

ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650

cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700

gggtttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750

ctcaaggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800

cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850

ggttcggcgg agcagtcctc agcccggccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
 gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
 tggttcagggt tgggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
 tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100  
 aaaaaaaaaa gaaa 1114

<210> 111  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
 Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
 1 5 10 15  
 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
 20 25 30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
 35 40 45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
 50 55 60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
 65 70 75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
 80 85 90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
 95 100 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
 110 115 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
 125 130 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
 140 145 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
 155 160 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
 170 175 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
 185 190 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg



200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys Arg	
215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys Gly	
230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe Val	
245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg	Ser Ser Pro Gln Pro Gly	
260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro	Gly Glu Ala Ala	
275	280	

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 112  
 gagctctgca acagctcctg gaag 24

<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 114  
 tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 gagctacca ggcgggtggt gtgcagcaag ctccgcgccg actccggacg 50

cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgcctgtct gctcaaggac 150  
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200  
ggatcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cggcacctgg acttggttcc cctcaagtct atccgagagt 400  
ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
gatgcagttt ggcgttaacc acctgggtca ctttctcttg aaaaacttgc 550  
tgttggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600  
tccttgccc atgttgctgg gcacatagac ttgacgact tgaactggca 650  
gacgaggaag tataacacca aagccgcta ctgccagagc aagctcgcca 700  
tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750  
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800  
cacgggcata catggctcca ccttctccag caccacactc gggcccatct 850  
tctggctgct ggtcaagagc ccgagctgg ccgccagcc cagcacatac 900  
ctggcctgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950  
actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000  
ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050  
gtgaggggagc agcccctccc cagataacct ctggagcaga ttgaaagcc 1100  
aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150  
ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200  
agtaggttct agggggcggg gctggccga gtggactggc ctgcaggtga 1250  
gcaactcccc gggtcttggc tggttccgtc tgctctgctg ccagcagggg 1300  
agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350  
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gcctgtcggg gaggggtcca aggtgctccg tgaagagcat gggcaagttg 1450

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgcatg 1500  
gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
ctgtctccca tgatgggtgtg gtacagcgag ctgttgtctg gctatggcat 1600  
ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650  
gagagcaggt gcaggtgtca tcccagattc aggcctctgca cggcatggag 1700  
tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
gctcattt 1808

<210> 116  
<211> 331  
<212> PRT  
<213> Homo sapiens

<400> 116  
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
1 5 10 15  
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
20 25 30  
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
35 40 45  
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
50 55 60  
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
65 70 75  
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
80 85 90  
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
95 100 105  
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
110 115 120  
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
125 130 135  
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
140 145 150  
Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
155 160 165  
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
170 175 180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185					190					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgcctggca tgtggtcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200  
 cggtgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggcctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600  
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700  
 agatgccttg gatcacttg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac ccaaaactgg tgacctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgacctg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500  
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600  
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgctcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
 gggagaggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900  
ggcctgagag ggaagtttct ggagttcaga tactctctgt tggaacagg 1950  
acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
agcccaagca gggagtgtcc cctcccaga agcatatccc agatgagtgg 2150  
tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200  
tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr
				470					475					480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp
				485					490					495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His
				500					505					510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys
				515					520					525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser
				530					535					540

Ser Pro Glu Asp

<210> 119  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 119  
 ggggacagga gaccagaaa ggg 23

<210> 120  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 120  
 ggccaagtga tccaaggcat cttc 24

<210> 121  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 121  
 ctgggggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122  
 <211> 1778  
 <212> DNA  
 <213> Homo sapiens



<400> 122

gagatagggg gtctgggttt aagttcctgc tccatctcag gagccctgc 50  
tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgcg ggggagcgcc caggatgccg 200  
cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctct 400  
ggcgctcgtc atgttcatgg tctccttcat tgggtgtctg gcgtccctcc 450  
gtgacaaact gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550  
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgtctgt ggggggagga ctaccgagat tggagcaaga atcagtacca 700  
cgactgcagt gccctggac cctggcctg tgggtgccc tacacctgt 750  
gcatcaggaa caggacagaa gttgtcaaca ccatgtctgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcactacg tgcggggctg 850  
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
gcatcctctt gggcatcctg ctccccagt tctgggggt gctgctgacg 950  
ctgctgtaca tcaaccgggt ggaggacatc atcatggagc actctgtcac 1000  
tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
cgggatgctg cttgtgttac cccaattagg gccagcctg ccatggcagc 1100  
tccaacaagg accgtctggg atagcacctc tcagtcaaca tctgggggct 1150  
ggacagggct gcggccctc tgcccacact cagtactgac caaagccagg 1200  
gctgtgtgtg cctgtgtgta ggtcccaagg cctctgcctc cccagggagc 1250  
agagcctggg cctcccctaa gaggtttcc ccgaggcagc tctggaatct 1300  
gtgccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
ctacagggga gggagagcct gaggtctctc tcagggccca ttcatctct 1400

ggcagtgcct tggcgggtggt attcaaggca gttttgtage acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg aggggaagggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggtggc 1550  
 ctctttctcag cctcccaggt gccttgagcc ctcttgcaag ggcgggtgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650  
 gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcctttccc ccaaccagtt tgттаатcaa асаатааааа 1750  
 catgttttgt tttgttttta аааааааа 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly				

170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn	Thr Thr Glu Val Val Asn	
185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp	Lys Glu Arg Phe Ser Val	
200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys	Thr Asn Ala Val Ile Ile	
215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met	Ala Cys Ile Leu Leu Gly	
230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

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<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

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<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

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<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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ctctgtgggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150

tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

ggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350

acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc ccttgacat ggtggctgga ttcaacacgc ccctgggtcaa 450

gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500

tggacaccag tgcaagtggc ccaccccgcc tggctctcag tgactgtgcc 550

accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct 600

ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccacccctgc 650

ccaatctagt gaaaaaccag ctgtgtcccc tgatcaggc ttccttcaat 700

ggcatgtatg cagacctct gcagctgggtg aagggtgccca tttccctcag 750

cattgaaccgt ctggagtttg accttctgta tctgtccatc aagggtgaca 800

ccattcagct ctacctggg gccaaagttgt tggactcaca gggaaagggtg 850

accaagtggt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900

caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950

tggctgtgtg gctctctcca gaagaattca tggctctgtt ggactctgtg 1000

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aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150

ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200

cacctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
 cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
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 gaaaccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550  
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<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

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 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170		175		180
Ala Lys Gln Val	Met Asn Leu Leu Val	Pro Ser Leu Pro Asn Leu			
	185		190		195
Val Lys Asn Gln	Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn Gly			
	200		205		210
Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser Leu			
	215		220		225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys			
	230		235		240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser			
	245		250		255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu			
	260		265		270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser			
	275		280		285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu			
	290		295		300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His			
	305		310		315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp			
	320		325		330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr			
	335		340		345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu			
	350		355		360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu			
	365		370		375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr			
	380		385		390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp			
	395		400		405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp			
	410		415		420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu			
	425		430		435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu			
	440		445		450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys			

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
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Pro Val Ser Gln

<10> 129

<11> 2213

<12> DNA

<13> Homo sapiens

<400> 129

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aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgcctt 200  
gtgaaaagccc caccgagaaa ttactccggt atcgtcatgt tcaactgctct 250  
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ccaaacgggg tgatacatat gagttacagg tgccggggttt ttcagctgag 500  
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
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tttgtagctg aaacacacat tgttcttctg tttaatgggtg gagttacctt 850  
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ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050  
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gtatattttg tattacctct ttttttcaag tgattttaaat agttaatcat 1150  
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 aactactact ttgttttagt tagaaciaag ctcaaaacta ctttagttaa 1350  
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 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900  
 cagttagaaa aggactcctt ggccaggcgc agtgacttac gctgtaatc 1950  
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000  
 gaccatcttg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
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 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150  
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200  
 aaaaaaaaaa aaa 2213

> 130

> 335

> PRT

> Homo sapiens

> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
1				5				10					15	

Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln



20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met		
35	40	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys		
50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile		
65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys		
80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg		
95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp		
110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser		
125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg		
140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln		
155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val		
170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu		
185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met		
200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys		
215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg		
230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn		
245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His		
260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu		
275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys		
290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser		

	305	310	315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr			
	320	325	330
Ser Phe Leu Met Ser			
	335		

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300  
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 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450  
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 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250  
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 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
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 cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
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 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
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<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val	530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
tcccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
catcaccag tgtgacatct atagaccct tctgggctg ccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgaat ctccctcctg 400  
gctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450  
atcccagcc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500  
ttggaggcct cctgggatcc attcctgttg cctggaatct tcatgggac 550  
ctacgggact ctactcacc actggtgcct gacagcatga aatttgagat 600  
tggagaggct cttaacttgg gcattatttc ttcctgttc tccctgatag 650  
ctggaatcat cctctgttt tctgctcat ccagagaaa tgcctccaac 700  
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gcttggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850  
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gctccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100  
agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
ccccaaaccc actaatcaca tccactgac tgacctctg tgatcaaaga 1200  
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250  
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tccatccac tcttggtatg 1350  
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp 30  
 20 25  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly 45  
 35 40  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly 60  
 50 55  
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala 75  
 65 70  
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile 90  
 80 85  
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr 105  
 95 100  
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala 120  
 110 115  
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro 135  
 125 130  
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro 150  
 140 145  
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr 165  
 155 160  
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile 180  
 170 175  
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr 195  
 185 190  
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg 210  
 200 205

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 220 225

Leu Thr Gly Tyr Val  
 230

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 cttegetect gcttatgtgt cagtctgtct cctcctcttg tgtccaagg 100  
 aagtcacgc tcccgtggc tcagaacct ggctgtgcc gccggcacc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcga atgtgggtccc cctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaac 300  
 gattttgttg tgaagctgaa gggtcaggg gtgaattccc agtgccactc 350  
 atctcccatc tccagtaa at gtgaaagcag aagacgtttt cctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys



	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
				95					100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
				110					115					

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250  
 ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgca ctcagcccg accctggatg acaggctttg tcgcagtgtc 350  
 agctaattga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggtctggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataaatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggctgc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttctcg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250  
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300  
 tgcaggctct tgggcccctgt ggacaaagg cagcatgtga ccttctacaa 350  
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 caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500  
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700  
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ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
 ggcagcctcc aaccgccttg cccaggagct ggtgcggatg gacagcaaca 850  
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 atacccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950  
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 ctctccagg ccccgagac gtcttcttcc catccctgga cctgtccct 1050  
 gaetctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggct ggctctgtga 1150  
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 gatactgtga catccagaa gccagcccc tcaacccctc tggatgctac 1250  
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
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 ccccgtaggc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550  
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 ggaagggtga gtggagaggg gcacctgcc cccgccctcc ccatccccta 1900  
 ctcccaactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccacctggg acattctga gtatgaagcg ggatgctatt aaaaactaca 2000  
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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	
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				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp			
	290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile			
	305	310	

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc cttctctgcc ctcttttctt gccaccgct gcttcttggc 150  
 ccttctccga ccccgctcta gcagcagacc tcttggggtc tgtgggttga 200  
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 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300  
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 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
 cagtcgctcc atgggtgag acatcctcag gatccatgtt ccagtgtatc 900  
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 ctctgagctt catcctcgc cacttcagac ccaagggagc aggcagcaca 1000  
 actgtcaaga tcgtctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
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tgggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
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 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctcgctccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
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 gaaggctact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<110> 142  
 <111> 451  
 <112> PRT  
 <113> Homo sapiens

<110> 142  
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 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp  
 20 25 30  
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser  
 35 40 45  
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg  
 50 55 60  
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His  
 65 70 75  
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln  
 80 85 90  
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg  
 95 100 105  
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His  
 110 115 120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	290	295	300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	305	310	315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	320	325	330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	335	340	345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	350	355	360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	365	370	375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	380	385	390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro  
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala  
 425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys  
 440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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 cttgcggaaa atgctgatct cagtcgcaat gctggjcgca ggggctggcg 150  
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 ttttaaggtec gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
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Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30



Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln	
				35					40					45	
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu	
				50					55					60	
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala	
				65					70					75	
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly	
				80					85					90	

Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Lys Met Leu Pro Leu Leu Glu Val Ala	Glu Lys Glu Arg Glu Ala	
65	70	75
Leu Arg Thr Glu Ala Asp Thr Ile Ser	Gly Arg Val Asp Arg Leu	
80	85	90
Glu Arg Glu Val Asp Tyr Leu Glu Thr	Gln Asn Pro Ala Leu Pro	
95	100	105
Cys Val Glu Phe Asp Glu Lys Val Thr	Gly Gly Pro Gly Thr Lys	
110	115	120
Gly Lys Gly Arg Arg Asn Glu Lys Tyr	Asp Met Val Thr Asp Cys	
125	130	135
Gly Tyr Thr Ile Ser Gln Val Arg Ser	Met Lys Ile Leu Lys Arg	
140	145	150
Phe Gly Gly Pro Ala Gly Leu Trp Thr	Lys Asp Pro Leu Gly Gln	
155	160	165
Thr Glu Lys Ile Tyr Val Leu Asp Gly	Thr Gln Asn Asp Thr Ala	
170	175	180
Phe Val Phe Pro Arg Leu Arg Asp Phe	Thr Leu Ala Met Ala Ala	
185	190	195
Arg Lys Ala Ser Arg Val Arg Val Pro	Phe Pro Trp Val Gly Thr	
200	205	210
Gly Gln Leu Val Tyr Gly Gly Phe Leu	Tyr Phe Ala Arg Arg Pro	
215	220	225
Pro Gly Arg Pro Gly Gly Gly Gly Glu	Met Glu Asn Thr Leu Gln	
230	235	240
Leu Ile Lys Phe His Leu Ala Asn Arg	Thr Val Val Asp Ser Ser	
245	250	255
Val Phe Pro Ala Glu Gly Leu Ile Pro	Pro Tyr Gly Leu Thr Ala	
260	265	270
Asp Thr Tyr Ile Asp Leu Val Ala Asp	Glu Glu Gly Leu Trp Ala	
275	280	285
Val Tyr Ala Thr Arg Glu Asp Asp Arg	His Leu Cys Leu Ala Lys	
290	295	300
Leu Asp Pro Gln Thr Leu Asp Thr Glu	Gln Gln Trp Asp Thr Pro	
305	310	315
Cys Pro Arg Glu Asn Ala Glu Ala Ala	Phe Val Ile Cys Gly Thr	
320	325	330
Leu Tyr Val Val Tyr Asn Thr Arg Pro	Ala Ser Arg Ala Arg Ile	

335	340	345
Gln Cys Ser Phe Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg Ala	
350	355	360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser Leu	
365	370	375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp Gly	
380	385	390
Tyr Gln Ile Val Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu Glu	
395	400	405

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
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 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
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 aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

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Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala	20	25	30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys	35	40	45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe	50	55	60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe	65	70	75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp	80	85	90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr	95	100	105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser	110	115	120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly	125	130	135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile	140	145	150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg	170	175	180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu	185	190	195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His	200	205	210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp	215	220	225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu	230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys	245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys			

290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val		
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp		
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His		
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr		
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr		
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe		
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg		
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn		
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu		
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu		
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu		
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 151  
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
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aatgaatggc ggaagcgagc gcgccatgag gagcctgccg agcctgggcg 150  
gcctcgccct gttgtgctgc gcgcgcgcgc cgcgcgcgt cgcctcagcc 200  
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro  
245 250 255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tgggtggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

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 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
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                     20                    25                    30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
                     35                    40                    45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
                     50                    55                    60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
                     65                    70                    75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
                     80                    85                    90  
 Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
                     95                    100                    105  
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
                     110                    115                    120  
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
                     125                    130                    135  
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
                     140                    145                    150  
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln  
                     155                    160

<210> 159

<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159

aacagacgtt ccctcgccgc cctggcacct ctaaccccag acatgctgct 50  
gctgctgctg ccctgctct gggggaggga gagggcgga ggacagaaa 100  
gtaaactgct gacgatgcag agttccgtga cggcgcagga aggcctgtgt 150  
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacc 200  
tggcccagta gttcatggct actggttccg ggaaggggccc aatacagacc 250  
aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaggag 300  
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcacc agagatgcc gaagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600  
ccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650  
gcccaggac catggcacc gcctcacctg tcaggtgacc ttccctggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750  
cagaacttga ccatgactgt ctccaagga gacggcacag tatccacagt 800  
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgc 850  
tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900  
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950  
ggctgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100  
tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttctgtgtag 1150  
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250  
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgcccc ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttccaga tggtaagcc ttgggactcg cggggacagg aggccactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
 1 5 10 15  
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
 20 25 30  
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
 65 70 75  
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
 80 85 90  
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
 95 100 105  
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg  
 110 115 120  
 Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu  
 125 130 135  
 Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile  
 140 145 150  
 Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser  
 155 160 165  
 Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp  
 170 175 180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala	410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser	425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu	440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg	455	460	

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 acctgtttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgccca ggaaggacca ctacatcttt tactgcaaag accagcacca 400  
 tggggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 aactaggca gcccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctc 650  
 gctccacccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
     1                    5                    10                    15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
                     20                    25                    30  
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
                     35                    40                    45  
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
                     50                    55                    60  
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
                     65                    70                    75



Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
				155					160					165	
Cys	Val	Pro	Glu	His											
				170											

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 165  
 gtccctccgga aagtccttat c 21

<210> 166  
 <211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gactagtgtt cgggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
cagggactg gtactgaag gccatggtg tcgataagga ctttcaggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
ctgtccttca ccttgaggga ggaggatgc acagggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169  
gttcgcaga tgcagaggtt gaggtggctg cgggactgga agtcacggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgctcc tccccctccc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgc agctcactc 200  
ccagccctgg caggcagccc tgttcgagaa gacgggcta ctctgtgggg 250  
cgacgtcat cgcgccaga tggctcctga cagcagccca ctgcctcaag 300  
ccccgtaca tagttacct ggggcagcac aacctcaga aggaggaggg 350  
ctgtgagcag acccgacag ccactgagtc ctccccccac ccggcttca 400  
acaacagct cccaacaaa gaccacgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cactgggct gtgcgacccc tcacctctc 500

ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
 gcacgtccag cccccagtta cgcctgcctc acaccttgcg atgcgccaac 600  
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
 cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccagggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
 attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800  
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900  
 tgggtgtttgg ttcctgttca ctctgtta atagaaaccct aagccaagac 950  
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100  
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu
1				5					10					15
Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro
				20					25					30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
				35					40					45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
				65					70					75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
				80					85					90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
				95					100					105

Asp His Arg Asn Asp Ile Met Leu Val	Lys Met Ala Ser Pro Val
110	115 120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys	
125	130 135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr	
140	145 150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn	
155	160 165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly	
170	175 180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly	
185	190 195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn	
200	205 210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala	
215	220 225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val	
230	235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn	
245	250

<210> 171  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 171  
 ggctgcggga ctggaagtca tcggg 25

<210> 172  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 172  
 ctccaggcca tgaggattct gcag 24

<210> 173  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 173  
tctctgggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 175  
cgtgtagaca ccaggctttc gggtg 25

<210> 176  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 176  
cccttgatga tcctggtc 18

<210> 177  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 177  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 178  
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 179  
gagcagtggt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50  
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100  
aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150  
agaaaactgc tctaagacaa gcaagaagg agacctaata aatgcccatt 200  
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250  
caaaatgaag gccaccccaa atggtttggt cttgggtgtg ggcaagtcac 300  
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350  
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400  
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
tgtgacaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500  
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
gaatttgaaa aagatgagaa gccacgtgac aagtcataac aggatgcagt 600  
tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750  
agtcactttt ctccaagttg tatttgctat tttcccta tgagaagata 800  
ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
ttgcaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
aaaaaaa 907

<210> 180  
<211> 222  
<212> PRT  
<213> Homo sapiens

<400> 180  
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	
				20					25					30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	
				35					40					45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	
				50					55					60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	
				65					70					75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	
				80					85					90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	
				95					100					105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	
				110					115					120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	
				125					130					135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	
				140					145					150	
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	
				155					160					165	
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	
				170					175					180	
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	
				185					190					195	
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	
				200					205					210	
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				
				215					220						

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 182  
   gacatggaca atgacagg 18  
  
 <210> 183  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 183  
   cctttcagga tgtaggag 18  
  
 <210> 184  
 <211> 13  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 184  
   gatgtctgcc accccaag 18  
  
 <210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 185  
   gcatcctgat atgacttgtc acgtggc 27  
  
 <210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 186  
   tacaagaggg aagaggagtt gcac 24  
  
 <210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>



<223> Synthetic oligonucleotide probe

<400> 187

gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaacaaaa acttctctgtg ctaagtgcc 100

cccaaatgct tctgtgtca ataactca ctgcacctgc aacctggat 150

atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatcca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttcttg ggatccccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser  
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
65 70

<210> 190  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 190  
agggaccatt gcttcttcca ggcc 24

<210> 191  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
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<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
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cccatcccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500  
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 gctggggcat caccaaccac ccacggaacc cattcccga tctgtccag 600  
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<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
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 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
 35 40 45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
 50 55 60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
 65 70 75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
 80 85 90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
 95 100 105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
 110 115 120

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	200	205	210
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	215	220	225
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	230	235	240
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								245		

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

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ctcccgatct tgetgccctt cttgacacac tgtgatctct ctctctctca 650  
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<210> 196

<211> 150

<212> PRT

<213> Hcmo sapiens

<400> 196

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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
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Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
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<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

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<210> 198

<211> 1523

<212> PFT

<213> Hcmo sapiens

<400> 198

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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
					20				25				30	

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro	50	55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg	65	70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu	80	85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe	95	100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys	110	115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu	125	130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg	140	145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp	155	160 165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175 180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190 195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205 210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220 225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235 240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250 255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265 270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280 285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295 300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310 315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr		

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Lys Lys Leu Lys Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu Phe	
365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn Lys	
380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn Leu	
395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser Lys	
410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile	Gln Thr Leu His Leu Ala	
425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His	Leu Lys Trp Leu Ala Asp	
440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys Ser	
455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	

605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser	
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr	
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu	
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly	
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys	
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala	
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln	
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val	
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met	
740	745	750
Pro Lys Asp Val Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	
755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	
770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	
785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	
800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe	Asn Gly Leu Arg Ser Leu	
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Arg Val Leu Thr Leu His Gly Asn Asp	Ile Ser Ser Val Pro Glu	
830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	
845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	
860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	
875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
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Ser Tyr Lys Gly Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
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Gln Asn Pro Cys Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser	Cys Glu Cys Val Pro	Gly
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp	Asn Asp Asp Cys Val	Ala
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys	Val Asp Thr Ile Asn	Gly
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe	Ser Gly Pro Phe Cys	Glu
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln	Thr Ser Pro Cys Asp	Gln
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys	Ile Val Val Gln Gln	Glu
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe	Ala Gly Pro Arg Cys	Glu
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly	Lys Asp Ser Tyr Val	Glu
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln	Ala Asn Ile Ser Leu	Gln

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 atggagattc ctgccaactt gccg 24

<210> 200  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 200  
 ttgttgcat tgaggaggag cagc 24

<210> 201  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 201  
 gagggcatcg togaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens

<400> 202  
 ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
 gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgctt tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
 cgggcattct gacctcatt ggctgcctgg tcaagggcgc cgagtcctaaa 200  
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
 agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
 gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400  
 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
 cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
 cctgtgtcat cttgtcccggt ttctcccaa tattccttct caaacttga 700  
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750  
 gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr	15
1				5					10						
Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile	30
				20					25						
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly	45
				35					40						
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr	60
				50					55						
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe	75
				65					70						
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu	90
				80					85						
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp	105
				95					100						
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr	120
				110					115						



Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaaacctgg caaaaatatt ctcgagggct ggccctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

caggccattt gcatcccaact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250  
agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tctgtctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600  
catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtga 650  
acattatcag gaattgaaga aaatggtcca acagtcgac cttggccagt 700  
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750  
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cggtgcactt ctcagaagca atagaaaagt tcatccgtga 950  
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
aaaaattttc cctgaagca ttacagAAC agctctaccg atatgttacc 1050  
aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
ttatggattg tagaccagct tttgaaacca aaaaagaaac ctagaatcta 1150

atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaagtgg 1300  
 tgtcattcca tgttcagcag agtatatttaa ttatatatttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450  
 ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcaactgtcat ctggttaggga atttttgttt gtctgtctt tgcttgatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 210  
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly  
 1 5 10 15  
 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val  
 20 25 30  
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His  
 35 40 45  
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg  
 50 55 60  
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly  
 65 70 75  
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val  
 80 85 90  
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val  
 95 100 105  
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro  
 110 115 120  
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu  
 125 130 135  
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala  
 140 145 150  
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg		
170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val		
185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe		
200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val		
215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu		
230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly		
245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu		
260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg		
275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg		
290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr		
305	310	315
Arg Tyr Val Thr Lys Leu Leu Val		
320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50

cttcgcgata ttccgccgta ccttcttgct ggcgttggtg ggagccgtgc 100

tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150

ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200

tttgcgatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250

ccttctggtt tggcaggcgc ctcgtgggta gtttgggcac tggtgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctectac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tctgttact ccagagaaaa 1000  
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tggtaactta ggatcctaact acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggaatt 1250  
 ctccaggaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtaacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggaac actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1					5				10					15

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala	20	25	30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu	35	40	45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn	50	55	60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg	65	70	75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His	80	85	90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys	95	100	105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn	110	115	120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu	125	130	135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu	140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290	295	300

Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val  
 305 310 315  
 Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu  
 320 325 330  
 Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln  
 335 340 345  
 Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg  
 350 355 360  
 Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro  
 365 370 375  
 Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp  
 380 385 390  
 Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly  
 395 400 405  
 Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr  
 410 415 420  
 Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val  
 425 430 435  
 Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
 440 445 450  
 Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggcttg tgccctctcg ctctctgacg ctctggcgc atctgggtgt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200  
 ctctcacgtt caccocccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600  
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgtttttag tagtaacattaag acttatatac agtttttaggg gacaattaa 750  
 aaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu 15  
 1 5 10  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp 30  
 20 25  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu 45  
 35 40  
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr 60  
 50 55  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val 75  
 65 70  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His 90  
 80 85  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp 105  
 95 100  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu 120  
 110 115  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu 135  
 125 130  
 Lys Lys Lys Pro Phe 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccgaccc tgccgcctg ccactatgtc ccgcgcctct atgctgcttg 50



cctgggctct ccccgacctc ctctgactcg gagcggtcca ggagacagaa 100  
gacccggcct gctgcagccc catagtcccc cggaacgagt ggaaggccct 150  
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
tatcgcacac ggcgggcagc agctgcaaca ccccgacctc gtgccagcag 250  
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350  
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
tcattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450  
ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500  
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
aacctctctc caggcaacca gctctaccac ctcattcaga attggccaca 600  
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650  
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	15
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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	30
			20						25						
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	45
				35					40						
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	60
				50					55						
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	75
				65					70						
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	90
				80					85						
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	105
				95					100						
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	120
				110					115						

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217  
 <211> 1871  
 <212> LNA  
 <213> Homo sapiens

<400> 217  
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 tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150  
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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20				25						30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
 50 55 60  
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
 65 70 75  
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
 80 85 90  
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
 95 100 105  
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
 110 115 120  
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
 125 130 135  
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
 140 145 150  
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
 155 160 165  
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
 170 175 180  
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
 185 190 195  
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
 200 205 210  
 Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225  
 Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
 230 235 240  
 Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgcgcgcgc cgcgcgcgc cctgcagcgc tgcgcaccta gccgctagca 250  
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 agcgcagacc ggctgcggct gccacacgc ctcaccatgg gctccgggcg 350  
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 ttgatgttaa atgjjaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
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 ttcaaataac ccatactctaa atttagtgca atatcttgtc ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgtc tggtatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 220  
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 20 25 30  
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
 35 40 45  
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
 50 55 60  
 Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
 65 70 75  
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
 80 85 90  
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
 95 100 105  
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
 110 115 120  
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
 125 130 135  
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
 140 145 150  
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
 155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
 170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
 185 190 195

Phe Leu Val Phe Pro Leu  
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<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 221  
 acggctcacc atgggctccg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 aggaagagga gcccttgag tccg 24

<210> 223  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
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<210> 224  
 <211> 902  
 <212> DNA  
 <213> Homo sapiens

<400> 224  
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 tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
 ttctgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

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 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400  
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 gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750  
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ta 902

<110> 225

<111> 257

<112> PFT

<113> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	15
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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	30
				20					25						
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	45
				35					40						
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	60
				50					55						
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	75
				65					70						
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	90
				80					85						
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	105
				95					100						



Pro Gly Glu Thr Ala Pro Ser Met Arg	Leu Leu Ala Tyr Val Ser	110	115	120
Gly Leu Gly Phe Gly Ile Met Ser Gly	Val Phe Ser Phe Val Asn	125	130	135
Thr Leu Ser Asp Ser Leu Gly Pro Gly	Thr Val Gly Ile His Gly	140	145	150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser	Ala Phe Met Thr Leu Val	155	160	165
Ile Ile Leu Leu His Val Phe Trp Gly	Ile Val Phe Phe Asp Gly	170	175	180
Cys Glu Lys Lys Lys Trp Gly Ile Leu	Leu Ile Val Leu Leu Thr	185	190	195
His Leu Leu Val Ser Ala Gln Thr Phe	Ile Ser Ser Tyr Tyr Gly	200	205	210
Ile Asn Leu Ala Ser Ala Phe Ile Ile	Leu Val Leu Met Gly Thr	215	220	225
Trp Ala Phe Leu Ala Ala Gly Gly Ser	Cys Arg Ser Leu Lys Leu	230	235	240
Cys Leu Leu Cys Gln Asp Lys Asn Phe	Leu Leu Tyr Asn Gln Arg	245	250	255

Ser Arg

<210> 226  
 <211> 3939  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser	1	5	10	15
Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln	20	25	30	
Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45	
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60	
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75	
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90	
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105	
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120	
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser				

125	130	135
Thr Leu Ser Pro Val Asn Thr Thr Tyr	Gln Leu Arg Val Ser Arg	
140	145	150
Met Asp Asp Phe Val Leu Arg Thr Gly	Glu Gln Phe Ser Phe Asn	
155	160	165
Thr Thr Ala Ala Gln Pro Gln Tyr Phe	Lys Tyr Glu Phe Pro Glu	
170	175	180
Gly Val Asp Ser Val Ile Val Lys Val	Thr Ser Asn Lys Ala Phe	
185	190	195
Pro Cys Ser Val Ile Ser Ile Gln Asp	Val Leu Cys Pro Val Tyr	
200	205	210
Asp Leu Asp Asn Asn Val Ala Phe Ile	Gly Met Tyr Gln Thr Met	
215	220	225
Thr Lys Lys Ala Ala Ile Thr Val Gln	Arg Lys Asp Phe Pro Ser	
230	235	240
Asn Ser Phe Tyr Val Val Val Val Val	Lys Thr Glu Asp Gln Ala	
245	250	255
Cys Gly Gly Ser Leu Pro Phe Tyr Pro	Phe Ala Glu Asp Glu Pro	
260	265	270
Val Asp Gln Gly His Arg Gln Lys Thr	Leu Ser Val Leu Val Ser	
275	280	285
Gln Ala Val Thr Ser Glu Ala Tyr Val	Ser Gly Met Leu Phe Cys	
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Cys Trp Glu Asn Trp Arg Gln Lys Lys	Lys Thr Leu Leu Val Ala	
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Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
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Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
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Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
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Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
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Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	

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Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
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Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
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Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe					
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser					
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<211> 2848

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 229

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Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
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Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
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Glu Tyr Gln Leu Gln Val Thr Leu Glu	Met Gln Asp Gly His Val	105
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Ser Arg Gly Thr Arg Pro Gly Ile Pro	Phe Leu Phe Leu Glu Ala	150
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Ser Asp Arg Asp Glu Pro Gly Thr Ala	Asn Ser Asp Leu Arg Phe	165
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His Ile Leu Ser Gln Ala Pro Ala Gln	Pro Ser Pro Asp Met Phe	180
170	175	
Gln Leu Glu Pro Arg Leu Gly Ala Leu	Ala Leu Ser Pro Lys Gly	195
185	190	
Ser Thr Ser Leu Asp His Ala Leu Glu	Arg Thr Tyr Gln Leu Leu	210
200	205	
Val Gln Val Lys Asp Met Gly Asp Gln	Ala Ser Gly His Gln Ala	225
215	220	
Thr Ala Thr Val Glu Val Ser Ile Ile	Glu Ser Thr Trp Val Ser	240
230	235	
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245	250	
His His Met Ala Gln Val His Trp Ser	Gly Gly Asp Val His Tyr	270
260	265	
His Leu Glu Ser His Pro Pro Gly Pro	Phe Glu Val Asn Ala Glu	285
275	280	
Gly Asn Leu Tyr Val Thr Arg Glu Leu	Asp Arg Glu Ala Gln Ala	300
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Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu		
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Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met		
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Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val		
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Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile		
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Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro		
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Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu		
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Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr		
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Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val		
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Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser		
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His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly		
530	535	540
Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val		
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Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu		
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Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr		
575	580	585
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu		
590	595	600
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly		
605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		

650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser	665	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val	680	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr	695	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile	710	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val	725	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg	740	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val	755	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile	770	780
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 <212> PRT  
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 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
 65 70 75  
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
 80 85 90  
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
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 110 115 120  
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 125 130 135  
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 140 145 150  
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
 155 160 165  
 Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile  
 170 175 180  
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala  
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Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
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Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
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Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
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Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
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Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
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Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
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Tyr

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 <212> DNA  
 <213> Homo sapiens

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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
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 20 25 30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala  
 200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgaactgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatettac ctttatggag tactctttgc tgttggectc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

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 caactctgac tccagcaca cctccagtga ggccagcaca gccaccaact 1550  
 ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600  
 tccagcaca cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650  
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ctccccatag tgcattctact gcagtgagtg aggcaaagcc tggtaggggcc 1750  
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 cgtgggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
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 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950  
 gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000  
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgc 2050  
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 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150  
 tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200  
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250  
 acacgacaaa gagaagctgt gcttgccccg gggtaggtat ctagtctga 2300  
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30

Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60

Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90

Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105

Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	110	115	120
Thr Asn Ser Glu Ser Ser Thr Pro Ser	Ser Gly Ala Ser Thr Val	125	130	135
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser	Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser	Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser	Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr Ala	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr Ala	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser	His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val	Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro	His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His	Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser	Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggtgtgc tagc 24

<210> 246

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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tcctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
cctcattgag aaggtcattg aacggatcaa ccgagggctg agcaatgcag 200  
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 tacacca 957

<210> 248  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
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 1 5 10 15  
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
 20 25 30  
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
 35 40 45  
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
 50 55 60  
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
 65 70 75  
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
 80 85 90  
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
 95 100 105  
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
 110 115 120  
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
 125 130 135  
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
 140 145 150  
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
 155 160 165  
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
 170 175 180  
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249

<211> 23

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caatatgcac attgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 250

aagcttctct gcttccttc ctgc 24

<210> 251

<211> 43

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 251

tgacccatt gagaaggcca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> RNA

<213> Homo sapiens

<400> 252

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tgacctgac tcaactcagg tccggaggcg ggggcccccg gggcgactcg 150

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 gtgagactg acttcacag gacgtgcc cgtgttcagg ggctgtgaat 2800  
 gctcggagag ggtcaactgg acctccctc cgtctgtct ttcgtggaac 2850  
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\*0100\* 253  
 \*0110\* 837  
 \*0120\* PFT  
 \*0130\* Homo sapiens

\*0400\* 253  
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu  
 20 25 30  
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser  
 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu  
 80 85 90  
 Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr  
 95 100 105  
 Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys  
 110 115 120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile	125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly	140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn	155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp	170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala	185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe	200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro	215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe	230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly	245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu	260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile	275	280	285
Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp	290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp	305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro	320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr	335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val	350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys	365	370	375
Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690



Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val	710	720
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe	725	735
Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln	740	750
Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu	755	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr	770	780
Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro	785	795
Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile	800	810
Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg	815	825
Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val	830	835

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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 255  
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<400> 255  
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<210> 256  
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 <212> DNA  
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<221> unsure  
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<213> unknown base

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 ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500  
 attcctgttt tagctgaaga attgtattac atttggagag taaaaaactt 4550  
 gaaacgaaa aaa 4563

• C10 • 260

• C11 • 802

• C12 • PRT

• C13 • Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	250	255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	265	270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys				

275										280										285									
Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala	290	295	300																										
Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu	305	310	315																										
His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg	320	325	330																										
Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser	335	340	345																										
Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro	350	355	360																										
Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu	365	370	375																										
Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly	380	385	390																										
Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu	395	400	405																										
Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala	410	415	420																										
Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly	425	430	435																										
Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp	440	445	450																										
Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val	455	460	465																										
Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile	470	475	480																										
Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys	485	490	495																										
Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser	500	505	510																										
Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu	515	520	525																										
His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu	530	535	540																										
Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu	545	550	555																										
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu																													

560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
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Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
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Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
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Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe



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<210> 263  
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<223> Synthetic oligonucleotide probe

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<210> 264  
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 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345
Leu Leu Lys Val Tyr	350		

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 \*211\* 2403  
 \*212\* DNA

<212> Homo sapiens

<400> 266

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 aaa 2403

.110: 267  
 .111: 466  
 .112: PFT  
 .113: Homo sapiens

2400: 267  
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 20 25 30  
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

35	40	45
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His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser 65 70 75		
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp 80 85 90		
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr 95 100 105		
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile 110 115 120		
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly 125 130 135		
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile 140 145 150		
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala 155 160 165		
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg 170 175 180		
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile 185 190 195		
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu 200 205 210		
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu 215 220 225		
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu 230 235 240		
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile 245 250 255		
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp 260 265 270		
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys 275 280 285		
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys 290 295 300		
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro 305 310 315		
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		

320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly	Arg His Tyr Trp Glu Val	
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val	Thr Leu Ser Pro Asn Asn	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr	Glu His Leu Tyr Phe Thr	
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro	Pro Ser Thr Pro Pro Thr	
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu	Gly Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Leu Thr Cys	
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr	Ile Gln His Ala Met Tyr	
440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe	Ile Cys Pro Val Ser Trp	
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<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

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 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaagggaag 1900



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<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210

Trp Asp Gly Ser	His Arg Cys Gly Ala	Thr Leu Ile Asn Ala	Thr
215		220	225
Trp Leu Val Ser	Ala Ala His Cys Phe	Thr Thr Tyr Lys Asn	Pro
230		235	240
Ala Arg Trp Thr	Ala Ser Phe Gly Val	Thr Ile Lys Pro Ser	Lys
245		250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile	Val His Glu Lys Tyr	Lys
260		265	270
His Pro Ser His	Asp Tyr Asp Ile Ser	Leu Ala Glu Leu Ser	Ser
275		280	285
Pro Val Pro Tyr	Thr Asn Ala Val His	Arg Val Cys Leu Pro	Asp
290		295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp	Val Met Phe Val Thr	Gly
305		310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr	Ser Gln Asn His Leu	Arg
320		325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala	Thr Thr Cys Asn Glu	Pro
335		340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro	Arg Met Leu Cys Ala	Gly
350		355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys	Gln Gly Asp Ser Gly	Gly
365		370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp	Ile Trp Tyr Leu Ala	Gly
380		385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala	Lys Pro Asn Lys Pro	Gly
395		400	405
Val Tyr Thr Arg	Val Thr Ala Leu Arg	Asp Trp Ile Thr Ser	Lys
410		415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> FRT

<213> Homo sapiens

<400> 271

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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
			20					25					30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40					45	

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
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 tgccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgccctgctct 250  
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aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400  
cggtcacgat tgcgttttgc tgtttcotta tcattgtggg gatgttagga 450  
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cagtgaactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850  
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gtattatgat agaagggagc ctgggacaga ccaaatgatg tcttgaaga 1000  
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agcctgtcaa gaatctttga acacacatcc atggcaaca gctttaatac 1100  
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<210> 273

<211> 305

<212> PFT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	170	175	180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	185	190	195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	200	205	210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	215	220	225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	230	235	240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	245	250	255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	260	265	270
Ile	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	275	280	285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	290	295	300
Glu	Met	Glu	Glu	Leu											305		

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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ctctgacctg ctggccagcc aggcctgtg tgggaggcc ctctgctgc 150

cttggggtga caatctcagc tccagctac agggagaccg ggaggatcac 200

agagccagca tgttacagga tctgacagt gacaaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat cccatggag accttcagaa 300

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<210> 275  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 275  
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 35 40 45  
 Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
 50 55 60  
 Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
 65 70 75  
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
 80 85 90  
 His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
 95 100 105  
 Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
 110 115 120  
 Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
 125 130 135  
 Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
 140 145 150  
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
 155 160 165  
 Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
 170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu	185	190	195
Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser	200	205	210
Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys	215	220	225
Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His	230	235	240
Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala	245	250	255
Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu	425	430	

\*E10\* 276  
 \*E11\* 3143  
 \*E12\* DNA  
 \*E13\* Homo sapiens

<400> 276

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 agagactggt tattttttat taaaaatata aggccttaaaa aaa 3143

<210> 277  
 <211> 761  
 <212> PFT  
 <213> Homo sapiens

<400> 277  
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 20 25 30  
 Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr  
 35 40 45  
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly  
 50 55 60  
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr  
 65 70 75  
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln  
 80 85 90  
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala  
 95 100 105  
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn  
 110 115 120  
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn  
 125 130 135  
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala  
 140 145 150  
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser  
 155 160 165  
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro  
 170 175 180  
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser  
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg	200	205	210
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg	215	220	225
Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr	230	235	240
Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp	245	250	255
Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys	260	265	270
Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr	275	280	285
Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro	290	295	300
Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro	305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val	320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp	335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu	350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg	365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr	380	385	390
Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr	395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val	410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr	425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly	440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp	455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala	470	475	480

Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly	Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe	Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu	Val Ala	755	760	

<210> 278  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 278  
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<210> 279  
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<212> DNA  
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<220>  
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<400> 279  
gtctggctct ggtgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
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<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
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tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450



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 <C12> PRT  
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 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile  
 35 40 45  
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg  
 50 55 60  
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln  
 65 70 75  
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys  
 80 85 90  
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly  
 95 100 105  
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln  
 110 115 120  
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys  
 125 130 135  
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys  
 140 145 150  
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu	Phe Gly Leu Pro Ile Fro	
170	175	180
Leu Ser Tyr Val Fro Val Phe Arg Ser	Leu Leu Thr Asp His Met	
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe	Leu Met Phe Phe Ser Phe	
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser	Thr Phe Asp Asn Thr Ile	
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg	Fro Val Leu Ser His Leu	
230	235	240
Leu Leu Lys Ala Gln Leu Trp Phe Ile	Asn Ser Asp Phe Ala Phe	
245	250	255
Asp Phe Ala Arg Fro Leu Leu Pro Asn	Thr Val Tyr Val Gly Gly	
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr				
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp				
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu				
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala				
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Val Trp Trp Leu	Arg Gly Ala Arg Lys Val Lys Glu Thr				
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 283

tgacttttgcg cacctacccc aagj 24

<210> 284

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 284

ctagggtgggt ctccaaagag aggg 24

<210> 285

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 285

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<210> 286

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 286

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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn		
	80	85 90
Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu		
	95	100 105
Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val		
	110	115 120
Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn		
	125	130 135
Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val		
	140	145 150
Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala		
	155	160 165
Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser		
	170	175 180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
	185	190 195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu		
	200	205

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

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<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290

ctgtgtact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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 <211> 388  
 <212> FET  
 <213> Homo sapiens

<400> 292  
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 35 40 45  
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn  
 50 55 60  
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln  
 65 70 75  
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile  
 80 85 90  
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu  
 95 100 105  
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly  
 110 115 120  
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr  
 125 130 135  
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu  
 140 145 150  
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile  
 155 160 165  
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu  
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg	Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu	Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp	Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile	Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro	Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys	Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

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<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 294

cccacajaca cccatjacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 295

acgcatgaat tgtacaaagc aggtgatctt cgaggagggc tctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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 agctcaagtg atctgcctgc ttcagcctcc caaagtactg ggattacaga 1850  
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacaaa 1900  
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacaacta 1950  
 ccaggagagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 2000  
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 accctgtctc 2060

<210> 297  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 297  
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu  
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 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe  
 20 25 30  
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu  
 35 40 45  
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln  
 50 55 60  
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu  
 65 70 75  
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80	85	90
Val Ile Ile Leu Asn His Asn Phe Glu	Ile Asp Phe Leu Cys Gly	
95	100	105
Trp Thr Met Cys Glu Arg Phe Gly Val	Leu Gly Ser Ser Lys Val	
110	115	120
Leu Ala Lys Lys Glu Leu Leu Tyr Val	Pro Leu Ile Gly Trp Thr	
125	130	135
Trp Tyr Phe Leu Glu Ile Val Phe Cys	Lys Arg Lys Trp Glu Glu	
140	145	150
Asp Arg Asp Thr Val Val Glu Gly Leu	Arg Arg Leu Ser Asp Tyr	
155	160	165
Pro Glu Tyr Met Trp Phe Leu Leu Tyr	Cys Glu Gly Thr Arg Phe	
170	175	180
Thr Glu Thr Lys His Arg Val Ser Met	Glu Val Ala Ala Ala Lys	
185	190	195
Gly Leu Pro Val Leu Lys Tyr His Leu	Leu Pro Arg Thr Lys Gly	
200	205	210
Phe Thr Thr Ala Val Lys Cys Leu Arg	Gly Thr Val Ala Ala Val	
215	220	225
Tyr Asp Val Thr Leu Asn Phe Arg Gly	Asn Lys Asn Pro Ser Leu	
230	235	240
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr	Glu Ala Asp Met Cys Val	
245	250	255
Arg Arg Phe Pro Leu Glu Asp Ile Pro	Leu Asp Glu Lys Glu Ala	
260	265	270
Ala Gln Trp Leu His Lys Leu Tyr Gln	Glu Lys Asp Ala Leu Gln	
275	280	285
Glu Ile Tyr Asn Gln Lys Gly Met Phe	Pro Gly Glu Gln Phe Lys	
290	295	300
Pro Ala Arg Arg Pro Trp Thr Leu Leu	Asn Phe Leu Ser Trp Ala	
305	310	315
Thr Ile Leu Leu Ser Pro Leu Phe Ser	Phe Val Leu Gly Val Phe	
320	325	330
Ala Ser Gly Ser Pro Leu Leu Ile Leu	Thr Phe Leu Gly Phe Val	
335	340	345
Gly Ala Ala Ser Phe Gly Val Arg Arg	Leu Ile Gly Glu Ser Leu	
350	355	360
Glu Pro Gly Arg Trp Arg Leu Gln		

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 298  
 cttctctgtt ggtggacca tgtg 24

<210> 299  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 299  
 ggtacctcca tgctaacgag g 21

<210> 300  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 300  
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<210> 301  
 <211> 1334  
 <212> DNA  
 <213> Homo sapiens

<400> 301  
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 tgcctttagca ctggggcact tcttgcttat ttcttttgta ggaaaggggc 150  
 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200  
 cggccctggg ttagaaggga aggggaagata aacttttata caaatgggga 250  
 tagctggggg ctgagacctg cttctcagt aaaattctg ggatctgctt 300  
 ataccttctt ttctctaacc tggcatacco tgcttaaagc ctctcagggc 350  
 ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgtttctct 450  
 tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
 ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650  
 ttcccttttg cagcaactgc cactcagttg tatctttatg tgcgtttgtg 700  
 gttgtatggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750  
 agggccaagg gcattgctgt gctgcccagg tatagtgctt acatgtggty 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggtctt gattcagtag 950  
 gccaggttg ggcattctta acaaaactcc acgtgatgct gatgctggtc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggtgagg caggctgac 1100  
 aactggagtc aggattttca gactagcctg gccacatgg tggaacccca 1150  
 tctgtactaa aaatacacaa attagctggg catggtggca catgctgtta 1200  
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aactgggag 1250  
 ggggaggttg cagtgagccg agatcaggcc actgtattcc aaccagggty 1300  
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15

His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25					30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



	65	70	75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr			
	80	85	90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln			
	95	100	105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu			
	110	115	120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr			
	125	130	135
Cys Gly Val Leu Leu Ser Phe Leu			
	140		

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 ttttccagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200  
 tttgtttctt tgtaactaga ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgtgg agcagtgcc tcccaactg tctcagctct ggaggcactg 400  
 actcgggcag tgcaggtagc ttagcctctt ggtagctgcg gctttcaagg 450  
 tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500  
 ggcgatggct cccactgcc aggcacagc cttgctgtag tcaatcactg 550  
 cctgggggcc aggacggcc gtggacacct gctcagaagc agtgggtgag 600  
 acatcacgt gcccgccat ctaacctttt catgtcctgc acatcacctg 650  
 atccatgggc taatctgaac tctgtccaa ggaaccaga gottgagtga 700  
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
 acgggaattg cattctctg gaacatgagg gaacgcgga ggaaagcaaa 800  
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
 gqaagggctg ccgatgggc atgacacact cgggactcac ctctggggcc 950  
 atcagacagc cgtttccgcc ccgacccacg taccagctgc tgaagggcaa 1000  
 ctgcaggccg atgtctcat cagccaggca gcagccaaaa tctgcgatca 1050  
 ccagccaggg gcagccgtct gggaaggajc aagcaaagt accatttctc 1100  
 ctccctctct tccctctgag aggcctctct atgtccctac taaagccacc 1150  
 agcaagacat agctgacagg ggctaattgc tcagtgttgg ccaggagggt 1200  
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacaaggaaa 1250  
 tgccctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
 ctcaatttaa atcatgttct agtaattgga gctgtccca agaccaaagg 1350  
 agctagagct tggttcaa at gatctccaag ggcccttata cccaggaga 1400  
 ctttgatttg aatttgaaac cccaaattca aacctaaaga ccagggtgat 1450  
 taagaatcag ttattgcggg gtgtgggtgg ctgtaatgcc aacattttgg 1500  
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccacatgg tgaaacctct gtctctacta aaaatacaaa aaaactagcc 1600  
 aggratgggt gtgtgtgct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
 ttccgctga gcaacacagc gagactctgt ctccagaaaa ataaaaaaag 1750  
 aattatgggt atttgtaa 1768

• 210 • 304

• 211 • 109

• 212 • PRT

• 213 • Homo sapiens

• 400 • 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5					10					15

Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	50		35		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

02100 305  
 02110 989  
 0212 DNA  
 0213 Homo sapiens

0300 305  
 gcgggcgcgc gagtcgcaga cctgtcccag gagctccagc tcacgtgacc 50  
 tgtcaactgc tccgcgcgc tctgtccgc gccatgacc agccggtgcc 100  
 ccggtctctc gtgcgcgcgc cgtgtgccc gggtccagcc gcactgggcg 150  
 ccgccttcgc cactggcctc ttctgggga ggcggtgcc cccatggcga 200  
 ggcgggcgag agcagtgcct gcttcccccc gaggacagcc gctgtggca 250  
 gtatctctctg agccgtctca tgcgggagca ccgggcgctg cgaagcctga 300  
 ggtgtgtgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
 caggccagc tcttggccaa cctggcgagg ctcatccagg ccaagaaggc 400  
 gctggacctg ggcaccttca cgggtactc ccgcctggcc ctggccctgg 450  
 cgtgtccgc ggcgggcgc gtggtgacct gcgaggtgga ccgcagccc 500  
 ccggagctgg gacggccct gtggaggcag gccgaggcgg agcacaagat 550  
 cgacctccg ctgaagccc ccttgagac cctggacgag ctgctggcgg 600  
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 aactgctcc cctactacga gcgtgcctg cagctgctgc gaccggagg 700  
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 cgaaagggga cgtggcgcc gagtgtgtgc gaaacctaaa cgaacgcctc 800  
 cggcgggag tcagggtcta catcagctc ctgcccctgg gcgatggact 850  
 caacctggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggtgccc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

```
<210> 306
<211> 262
<212> PET
<213> Homo sapiens
```

400: 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
				245					250					255

Leu Thr Leu Ala Phe Lys Ile  
260

02100 307  
02110 2272  
0212 DNA  
0213 Homo sapiens

0400 307  
ccgcgcgcgc agccgcctacc gccgcctgcag ccgccttccg cggcctgggc 50  
ctctcgcgcgt cagcatgcc aacgccttca agcccgggga cttggtgttc 100  
gctaagatda agggctaccc tcaactggcct gccaggatcg acgacatcgc 150  
ggatgjcgcg gtgaagcccc caccacaaca gtaccacata tttttctttg 200  
gcacacacga aacagccttc ctgggaccca aggaactgtt cccctacgac 250  
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
agggctgtgg gagatccaga acaaccccc aagcagctac agcgccctc 350  
cgcacgtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
ggcagtgaag ctgacgagga cgatgaggac cggggggtca tggccgtcac 450  
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cagacaagag tagcacaac agtggcctga agaggaaagc gctgcgccta 550  
aaatgtcgg tctcjaaac agccccaaag gctccagcg acctggatca 600  
ggccagcgtg tcccatccg aagaggagaa ctgggaaagc tcatctgagt 650  
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cgggcgcac ggagjggccc tctgggggga cggaaaaaaa agaaggcgcc 750  
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agcgggtggc catggcgcgg tcggcgctct cctctctctc ttctctctcc 850  
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atcagtgagt ggaagcggcg ggacgaggcg cggajjcgcg agctggaggc 1050  
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agaaggagga gaagjagcg agggcgagc ggccjaccg cgggaggct 1150  
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gcccgtcaag aagcggggac gcaagggcgc gggccgggt ccccgctct 1250  
 cctctgactc cgagcccag gccgagctgg agagagaggg caagaaatca 1300  
 gccaagaagc cgcagctctc aagcacagag cccgccagga aacctggcca 1350  
 gaaggagaag agagtggggc ccgaggagaa gcaacagcc aagcccgta 1400  
 aggtggagcg gacccggaag cggcccgagg gcttctcgat ggacaggaag 1450  
 cttagagaaga agaaagagcc ctccgtgag gagaagctgc agaagctga 1500  
 cagtgcagtc aagtttgccc taaaagtcca cagcccgga gtgaagaggt 1550  
 gctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600  
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 gctggccggg gaggaggccc cccaggagaa ggcggaggac aagccagca 1850  
 ccgactcttc agcccagtg aatggcgagg ccacatcaca gaagggggag 1900  
 aggcagaggg acaaggagca cgaggajgtt cgggactcgg agjaggggcc 1950  
 aaggtgtggc tctctgaag acctgcacga cagcgtacgg gagggtcccg 2000  
 acctggacag gctggggagc gaccggcagg agcgcgagag ggcacggggg 2050  
 cactcggagg cctggacga ggagagctga gcggggggca gccaggccca 2100  
 gcccccggcc gagctcaggg tgcctctctc cttcccccgc tcgcaggaga 2150  
 gcagagcaga gaactgtggg gaacgtgtg ctgtttgtat ttgttccctt 2200  
 gggttttttt ttctgcta atttctgtga ttccaacca acatgaaatg 2250  
 actataaacg gttttttaat ga 2272

<210> 308  
 <211> 671  
 <212> PFT  
 <213> Homo sapiens

<400> 308  
 Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met  
 1 5 10 15  
 Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp  
 20 25 30  
 Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35	40	45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro 50 55 60		
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys 65 70 75		
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala 80 85 90		
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala 95 100 105		
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp 110 115 120		
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala 125 130 135		
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser 140 145 150		
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser 155 160 165		
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala 170 175 180		
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu 185 190 195		
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala 200 205 210		
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys 215 220 225		
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser 230 235 240		
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser 245 250 255		
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val 260 265 270		
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro 275 280 285		
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser 290 295 300		
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu 305 310 315		
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg		

320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435
Pro Glu Glu Lys Gln Gln Ala Lys Pro	Val Lys Val Glu Arg Thr	
440	445	450
Arg Lys Arg Ser Glu Gly Phe Ser Met	Asp Arg Lys Val Glu Lys	
455	460	465
Lys Lys Glu Pro Ser Val Glu Glu Lys	Leu Gln Lys Leu His Ser	
470	475	480
Glu Ile Lys Phe Ala Leu Lys Val Asp	Ser Pro Asp Val Lys Arg	
485	490	495
Cys Leu Asn Ala Leu Glu Glu Leu Gly	Thr Leu Gln Val Thr Ser	
500	505	510
Gln Ile Leu Gln Lys Asn Thr Asp Val	Val Ala Thr Leu Lys Lys	
515	520	525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp	Val Met Glu Lys Ala Ala	
530	535	540
Glu Val Tyr Thr Arg Leu Lys Ser Arg	Val Leu Gly Pro Lys Ile	
545	550	555
Glu Ala Val Gln Lys Val Asn Lys Ala	Gly Met Glu Lys Glu Lys	
560	565	570
Ala Glu Glu Lys Leu Ala Gly Glu Glu	Leu Ala Gly Glu Glu Ala	
575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro	Ser Thr Asp Leu Ser Ala	
590	595	600
Pro Val Asn Gly Glu Ala Thr Ser Gln	Lys Gly Glu Ser Ala Glu	



605	610	615
Asp Lys Glu His Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro Arg	
620	625	630
Cys Gly Ser Ser Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro	
635	640	645
Asp Leu Asp Arg Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg Ala	
650	655	660
Arg Gly Asp Ser Glu Ala Leu Asp Glu	Glu Ser	
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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
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Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile	
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Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His	
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Pip					
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Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp 575	580	585
Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val 590	595	600
Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro 605	610	615
Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly 620	625	630
Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys 635	640	645
Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser 650	655	660
Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr 665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu 680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu 695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu 710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp 725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp 740	745	750
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<213> Artificial Sequence

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\*223> Synthetic oligonucleotide probe

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\*220>  
\*223> Synthetic oligonucleotide probe

\*400> 312  
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\*210> 313  
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\*213> Homo sapiens

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 (212) PRT  
 (213) Homo sapiens

(400) 315  
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 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg  
 50 55 60  
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu  
 65 70 75  
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 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser  
 95 100 105  
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp  
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 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu  
 125 130 135  
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro  
 140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp	155	160	165
Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu	170	175	180
Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu	185	190	195
Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser	200	205	210
Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu	215	220	225
Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln	230	235	240
Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu	245	250	255
Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly	260	265	270
Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu	275	280	285
Glu Leu Leu Gly Pro Pro Gly Pro Pro Gln Leu Ser Asp Pro Glu	290	295	300
Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala	305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly	320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro	335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Pro Ala Lys Ala	350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr	365	370	

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 <212> DNA  
 <213> Homo sapiens

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aagaaaa 4407

0210 317

0211 837

0212 PRT

0213 Homo sapiens

0400 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
			140						145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
			155						160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
			170						175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
			185						190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
			200						205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
			215						220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
			230						235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	150	255
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260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala		
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn		
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	419
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro		
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val		



530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly		
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Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn		
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Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu		
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Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe		
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Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro		
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Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr		
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Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser		
635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala		
650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys		
665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly		
680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile		
695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro		
710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser		
725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys  
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&lt;210&gt; 318

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; Synthetic oligonucleotide probe

&lt;400&gt; 318

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&lt;210&gt; 319

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; Synthetic oligonucleotide probe

&lt;400&gt; 319

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&lt;210&gt; 320

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; Synthetic oligonucleotide probe

&lt;400&gt; 320

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&lt;210&gt; 321

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

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0210 - 322

0211 - 317

0212 - PET

0213 - Homo sapiens

0400 - 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80										85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe					
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Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys					
				110					115					120					
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro					
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Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe					
				140					145					150					
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn					
				155					160					165					
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn					
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Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu					
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Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala					
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				215					220					225					
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu					
				230					235					240					
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe					
				245					250					255					
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg					
				260					265					270					
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly					
				275					280					285					
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys					
				290					295					300					
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly					
				305					310					315					

Arg Val

<210> 313

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

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<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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0210 • 326  
 0211 • 261  
 0212 • PFT  
 0213 • Hemo sapiens

0400 • 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
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Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
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Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170				175					180	
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185				190					195	
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200				205					210	
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215				220					225	
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230				235					240	
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
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<210> 327

<211> 3010

<212> DNA

<213> Homo sapiens

<400> 327

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gtgggcacag tggctgtcac tgtcatgctt cagtggagag tgtgggcctt 200
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<210> 328

<211> 225  
 <212> PFT  
 <213> Homo sapiens

<400> 328

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				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
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Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<210> 329  
 <211> 1315  
 <212> DCA  
 <213> Homo sapiens

<400> 329

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- 210 • 330
- 211 • 220
- 212 • PRT
- 213 • Homo sapiens

<400> 320

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Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
              35              40              45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
              50              55              60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
              65              70              75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
              80              85              90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
              95              100              105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
              110              115              120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
              125              130              135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
              140              145              150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
              155              160              165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
              170              175              180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
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Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
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Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
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<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210 - 332

<211 - 173

<212 - PRT

<213 - Homo sapiens

<400 - 332

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Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30
Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu

35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val		
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<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agaagtatcc agtggtyggc atcccttgc ccctcacata cctaccagtt 200
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<210> 334  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 334  
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                   20                  25                  30  
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
                   35                  40                  45  
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
                   50                  55                  60  
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
                   65                  70                  75  
 Arg Val Gln Phe Leu His Asp Gly Ser Cys  
                   80                  85

<210> 335  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<400> 335  
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cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
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Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
				20					25					30
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35					40					45
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr		
				140					145					

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

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tgaaggggtg ggtgatgagg tgaccgtcct ttctcgggtg cttgcctgac 150  
ttctgggtgct ggcccttgcc tgggtctcaa cgcacacgcg tgaggggggg 200  
gacctactgc ccagccgtc agggacccca accccatccc agccagcgc 250  
agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

ccccagcct gagacacaga ggtcaagctg cacagccaga gccacagcag 350  
gggttcacag caacaccgcc agcccggac tcccgcagg agcccctgt 400  
gctaaggctg aaattctca atgattcaga gcaggtggcc agggcctggc 450  
cccacgacac cattggctcc ttgaaaagga cccagtctcc cggccgggaa 500  
cagcaggtgc gactcatcta ccaaggggag ctgctaggcg acgacaccca 550  
gacccctgggc agccttcacc tccctccaa ctgcttctc cactgccaag 600  
tgtccagag agtcgtccc ccaatccc cctgcccgc ggggtccag 650  
ccgggcccct cggggtgga aatggcagc ctgctgtgc cctgtgtgt 700  
ctgtgtgttg ctgtgtgtt ggtactgcca gatccagta cggcccttt 750  
tccctgac cgcactctg ggcctggcg gcttcacct gctcctcagt 800  
tccctggcct ttgcctgta cggccctgag tgcctccgc gggcttggc 850  
aggttcgag gccctccgg accttgcct ccgcccgcg ggggagctg 900  
ctgctgccc aggcccgct cccggcctg cctctcccg ctgcccggg 950  
gccacgcct ggcgcgcaga ggactcccg gactggcgga ggccccgcc 1000  
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tgcactggga gtgggtcct cgggtccgg catctgtgt cgtgctctg 1100  
tccccgggca gagccgggc gccccgggg ccgctcttag tgtctctgg 1150  
tgggacccag ccgcctccaa tccctgacag ctccctgggc ttagttggg 1200  
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ttccccgga acccgtgag attaaagtaa ctgtgaagt ttaaaaaaa 1300  
aaaaaaaa 1310

<110> 338  
<111> 246  
<112> PRT  
<113> Homo sapiens

<400> 338  
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Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
20 25 30  
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

(210) 339  
 (211) 349  
 (212) DNA  
 (213) Homo sapiens

(400) 339  
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 atgacaaagg cgtactcat ctatttggtc agcagtttc ttgcctaaa 200  
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 ccttcccatt tacaactaaa actgaccaga gccacaggaa taaatgggtt 750  
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 tgttatttgt aaactgagga ccacaataaa gaaatcttta ttttatcg 849

(210) 340  
 (211) 148  
 (212) PRT  
 (213) Homo sapiens

(400) 340  
 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala  
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 Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val  
                   20                  25                  30  
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
                   35                  40                  45  
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
                   50                  55                  60  
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
                   65                  70                  75  
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
                   80                  85                  90  
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
                   95                  100                  105  
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
                   110                  115                  120  
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
                   125                  130                  135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

gcctcraagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcagggcgc gcatactgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtatgatgact gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccttaaata ggcagctc atcagtcgt gtgac 45

(210) 346

(211) 2575

(212) DNA

(213) Homo sapiens

(400) 346

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caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccgggggtaaa gggaggggaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtccctg tggttctctg attgtaagtg gaagcaggtc 300  
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttcag gtggaacaag caaccatgt tctctgcaa gcttgaagga 400  
gcttgagcg ggagaaagct aactgaaca tgacctgtg catttggcaa 450  
gttctagcaa catgtccta aggaagcgat acaggcacag accatgcaga 500  
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 tcagcagaat agctggtgac aggagccgag tggatatctc ggtgatagat 1400  
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 ctttcaaggc ctggctctgt ggtggctctg ttgaaacct tccctgtct 1700  
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 aagctgaga agccagactg catggaaagc ttgcagctgc aaaggagact 1900  
 ggggtgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
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 tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

(212) PRT

(213) Homo sapiens

(400) 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	



Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
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Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
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<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 348

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<210> 349

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagocaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 350

tatgtgcgtg cgagggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2324

<212> DNA

<213> Homo sapiens

<400> 351

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 cagtcctccc ttcccagcct ccccttgggc ctccctaact ccaactagga 2200  
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 caggttcttc cctccttctc actggttttt ccaacttct ccttcccttc 2400  
 ttccctggct cctaggctgt gatatatatt ttgtattat ctctttcttc 2450  
 ttctgtggt gatcatctg aattactgt ggatgtaagt tccaaaattt 2500  
 tccaaataaag cctttgcaag ataa 2524

(210) > 352  
 (211) > 243  
 (212) > PRT  
 (213) > Homo sapiens

(400) > 352  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15  
 Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
 20 25 30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Gln	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240
Leu Pro Lys																	

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
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 cgggcaggat ggcattctgt ctggccctgc gcatggcgt gctgctggtc 100  
 tccggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgccacg ctgtggaacg agccggccga gctgcccgtg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250  
 gcccccacgg tcgcccacgg acccgaggac agcacccggc aggagcggct 300  
 ggaccagggc ggccgggtgc tggggcccg ggtatcgcg gccatcgtga 350  
 tcgcccgcct gctggccacc tgggtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc ggcgcgggac 450  
 gggcgcgac tcggcaaaaa aaaaaaaaaa 480

#210 - 354

#211 - 121

#212 - PFT

#213 - Homo sapiens

#400 - 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5				10					15	
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20				25					30	
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35				40					45	
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50				55					60	
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65				70					75	
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80				85					90	
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95				100					105	
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110				115					120	

Ser

#210 - 355

#211 - 2134

#212 - DNA

#213 - Homo sapiens

#400 - 355

ggcgttggt tgggtggggc ctgaagggtg tggcgggagc agcgtcgttg 50  
 gttggcggc ggccggggcg gacgggcatg gccctgctgc tgtgcctggt 100

gtgootgacg ggggogctgg cccacggctg totgcaactg cacagcaact 150  
 tctccaagaa gttctccttc tacggcacc atgtgaaatt caagtcoctgg 200  
 tgggtggggg acatccccgt gtcaggggg ctgctcaccg actggagoga 250  
 cgacacgatg aaggagctgc aactggccat ccccgccaag atcacccggg 300  
 agaagctgga ccaagtggcg acagcagtg accagatgat ggatcagctg 350  
 taccagggga agatgtactt ccccggttat ttccccaacg agctgggaaa 400  
 catcttcggg gagcaggtgc aactcatcca gaacgcacac atcgaaaggc 450  
 aactggcacc aggcagctgg ggaggagggg agctctccag ggagggaccc 500  
 agoctagcac ctgaaggatc aatgcaccca ccccgggggg aactccctca 550  
 agtagccccc agaggogctg ggagtgttgc caccgacctc cctgaagtt 600  
 tgcctccatct cagctggggg gtcaacctgg ggaccttc cctccggggc 650  
 atggacacac atacatgaaa accaggccgc atcgactgtc agcacogctg 700  
 tggcatcttc cagtaogaga ccatctctg caacaaactg acagaactgc 750  
 aactggcctg ctttggtat aactggaggt agggctcagg catcaccccc 800  
 acccgtgcca gggccctact gtccctgggg tcccaggctc ccttgaggg 850  
 gggctccccg ccttcacact ggcgtcacc gggtagggcg gggccgtggg 900  
 ttcagggggg caccacttc aagcctgtgt cccacaggtc ctggggcag 950  
 tgggaagtac ctgtccaggg cctcctgaac tacataaata actggcaca 1000  
 gtaagtcccc tctcaaac aacacaggca gtgtgtgtat gtgagcaact 1050  
 cgtgggtgag tatgtgtgg gcacaggctg gctcctcag ctcccaagtc 1100  
 ctgagggggg tcccaggag gtggaaacct aaccagctc tgccaggag 1150  
 gggctgcag tcttttctc cctcaaggt ctcagacct cagctggagg 1200  
 cgggcactct tctaaaggg tcccacagg gtctgttcc accccatccc 1250  
 aggtctgtgg ccagagcctg ggagggttc ctacgatgt taggggtgac 1300  
 ccattggagg gctgactgc ccacattgac ttccagacag gacacgagca 1350  
 tgaggtaagg ccgcctgac ctggacttca gggggagggg gtaaaggag 1400  
 agaggagggg ggcaggggg tctctagat cagtggggg actgcagggt 1450  
 gggctctccc tatacctgg acacctgct gatgtcact ctgcaaccac 1500

accatgtgg tggtttcacg aacagaccac gctctcttgc cttctcctgg 1550  
 cctggggacac acagagccac cccggccttg tgagtgaacc agagaaggga 1600  
 ggctctggga gaaggggtgc tctgaagcca acaccagcgt gcggcgccct 1650  
 gcacacccct cggacatccc aggcacgagg gtgtcgttga tgtggccaca 1700  
 cataggacca caagtcaccg ctgggaggag aggcctgggg cccccaggga 1750  
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 gcagcctggt atgcgcagcc ttaagggtgc tggagccccc acacttgggc 1850  
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 gctgggcctg cccagggcca acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggtctgtc ctgcctcagg acccctctc 2000  
 cgaccccgga cagagctgag ctggccaggc ccaggagggc gggagggagg 2050  
 gaatgggggt ggggtgtgag cagcatcagc gctggggcag gtcgcagag 2100  
 ctgggggatg tgattaaagt cctgatgtt tctc 2134

\*210 - 356  
 \*211 - 157  
 \*212 - FET  
 \*213 - Homo sapiens

\*400 - 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln



125

130

135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro  
 140 145 150

Ser Pro Arg Gly Asp Leu Pro  
 155

1110: 357

1111: 1536

1112: DNA

1113: Homo sapiens

1400: 357

agcaggagca ggagagggac aatggaagct gcccggtcba ggttcattgt 50  
 cctcttattt ctcttcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
 ttgagaaaac ctccagatggc cctggctgctg cccaggaaac cactgggctc 150  
 acaagatgtc cagctgcacat ggaattcatt gctgcacatg aggtggatgt 200  
 catagggctc ttccaggatt tagaaataac agcagtgccc ataactacata 250  
 gcatgggtga aaaattccca gggtgtctat ttgggacacg cactgattct 300  
 gaggtttctg cacaactaaa cctcactggg aacacacatct gctctttctg 350  
 ccttgtagac aatgaacaac tgaatttaga ggaaggaagc attgaaagca 400  
 ttgatgcac caaattgagc cgttttcatt agatcaacag cctccacatg 450  
 gtgacagagt acaacccgtg gactgtgatt gggctattca acagcgtaat 500  
 ccagattcat ctctctctga taatgaacaa ggctccacca gactatgaag 550  
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
 ctcttttatt tggtagacag tggtagaaa gaaaatggga aggtgatata 650  
 atttttcaaa ctaaaaggagt ctcaactgcc agctttggca atttaccaga 700  
 ctctagatga cagctgggat acactgacca cagcagaagt ttccgtagag 750  
 catgtgcaca acttttgtga tggattcta agtggaaaat tgttgaaaga 800  
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaaact tgaattctcc 850  
 ttggaaacta atatggccaa gtatctactt tatgcacaagt aaaaaggcac 900  
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgcacaac 950  
 acacacacac gcaagtgcac acaagcagc agcgtgcac acacacacgc 1000  
 gacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
 tctcttcttc ctctctttta atttcatata ctcaactcct atccaatttc 1100

atttattatcg tgcattcata ctctgtaagc ccattctgtaa cacacctaga 1150  
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200  
 cttagagaaag attgttccaa ttgttcattt aatatcaagt ttgtatactg 1250  
 cacatgactt acacacacaa tagttcctgc tcttttaagg ttacctaaagg 1300  
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaaacca aaggatgggt ttaaaccact ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggcgtgtct caagtccttg aactcagcag aaatagacca 1450  
 tgtgaaaact ccattgcttg ttagcatctc caactcccta tgtaaatcaa 1500  
 caactgcat aataaataaa aggcaatcat gttata 1536

0010 • 358  
 0011 • 273  
 0012 • PRT  
 0013 • Homo sapiens

0400 • 358  
 Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu  
 1 5 10 15  
 Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser  
 20 25 30  
 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp  
 35 40 45  
 Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val  
 50 55 60  
 Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu  
 65 70 75  
 His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser  
 80 85 90  
 Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr  
 95 100 105  
 Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu  
 110 115 120  
 Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe  
 125 130 135  
 Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val  
 140 145 150  
 Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu  
 155 160 165

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				176					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Gln	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 359

ccagcagtgcc ccatactcca tagg 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgacgagtggtg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gctctacgga aactttctgt gtgg 24

(C10): 362  
 (C11): 50  
 (C12): DNA  
 (C13): Artificial Sequence

(C20):  
 (C21): Synthetic oligonucleotide probe

(C40): 362  
 attcccaagc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

(C10): 363  
 (C11): 1777  
 (C12): DNA  
 (C13): Homo sapiens

(C40): 363  
 ggaagagcgc ggctgggacc ggagtgggga gggcgggcgtg gaggtgacac 50  
 ccgacccggg tggcggagag atcagaagcc tcttccccaa gccgagccaa 100  
 cctcaagcgg gaccggggct cagggacggc gggcgggcgg cggcgactgc 150  
 agtggctgga cgatggcagc gtccggcgga ggcggggcgg tgattgcagc 200  
 cccagcagc cggcgctggc tgtggctggg gctggcgggc ggccttgggc 250  
 ccttgacagc tggagtatca gccttggaag tatataccc aaaagaaatc 300  
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 tagtaagact ggggggttga cctcagtttc ctggagcttc cagccagagg 400  
 gggccagac tactgtgtcg ttttccact acctcccaagg gcaagtgtac 450  
 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
 tgacaagaaa gatgcacaa ccaacataga aaatatgcag tttatacaca 550  
 atggcactta tatctgtgat gtcaaaaaac ctctgacat cgttgtccag 600  
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 tccagtttgg gtagtggtag gcatagttac tgcctgtggc ctaggctctc 700  
 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
 aaaagggatt acaactggctg cagtaacatc gagagtttct caccagttaa 800  
 gcaggctcct cggaaagccc cctccgacac tgagggtctt gtaaagagtc 850  
 tgctttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900  
 tccggcgga atcacagtga caagattaac aagtcagagt ctgtgggtga 950  
 tgccgatata cgaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcac 1150  
 cctgatatga ggagccagt ttgcatgatg aaaagatggg atgattctac 1200  
 atatgtacc cttgtcttgc tgtttttgta cttctcttcc aggtcattta 1250  
 caattgggag atttcagaaa cttccttcc accatcattt agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
 ccttttaata taagggtta agactgatta gtcttagcat ttaactgtagt 1400  
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450  
 cagtatcagt accatttatt tgtctgcgc ttttaaaaaa taaccattgg 1500  
 ctatgcact tgaaaacaat ttgagaagtt tttttgaagt tctctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttaactttaag 1600  
 ttgcaacct tgaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaag gataaatgac gaaggcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtata ggtttta 1777

0210 - 364  
 0211 - 269  
 0212 - PET  
 0213 - Homo sapiens

0400 - 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5					10					15
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	95	100	105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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cgggctgacg ccccgggggg cttggcctca agctgcggac gacgoggggt 100
ccatcagcgc gcggggtgc cgcctctcgg ccacggctgg gtccgggggc 150
tcgggtgagg gctgggggtg gcgctcgggg tgaagtggc aggtgggctg 200
agggggcggg ccccgggcga gtcccccggg gcccgcgacc ctgaggcgtc 250
gcctctggcc gagccgcac aggagcagtc cctcgccccc tgggtctcgc 300
agaccccggc gcgcacctgc tccaggtgct tcgcacagag catcgagagc 350
agcccgagac tgtgcacag gatcaaggat gaggtggggc caccgggcac 400

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agtgggttga gttttctgtag atggaaaaga agtctgggtca gaagggttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaacaga gacagttatg 500  
 cgaattgcta gcacagcaa aagtctcacc atgggttgcctc ttgcccatt 550  
 gtgggaagca gggaaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgcacacaa 650  
 agattactga tttccatttt aagtgggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aaacttataa agccttgaag atgatgaaag 750  
 agaattgttc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgocggaa 850  
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
 ttagagaaaa gtttgaaaat tcaattgaat cctaagatt atttaaaaat 950  
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 caggaagaaa acgagccagt gatttacaat agagcaaggc aaatgaatac 1150  
 cttctgtgtt gctagctat atgcctctt aacactattt tattaattaa 1200  
 aagtcacatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250  
 gagcttttct acatgtctgt ttctcctct gtaaagtgaa ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PFT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
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Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25						30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55						60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345



Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
 350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
 365 370

\*010\* 367

\*011\* 30

\*012\* DNA

\*013\* Artificial Sequence

\*020\*

\*023\* Synthetic oligonucleotide probe

\*400\* 367

tggaagagaa gtctggtcag aaggtttagg 30

\*010\* 368

\*011\* 25

\*012\* DNA

\*013\* Artificial Sequence

\*020\*

\*023\* Synthetic oligonucleotide probe

\*400\* 368

catitggctt cattctcctg ctctg 25

\*010\* 369

\*011\* 27

\*012\* DNA

\*013\* Artificial Sequence

\*020\*

\*023\* Synthetic oligonucleotide probe

\*400\* 369

aaaacccag aacaactcat ttgcacc 28

\*010\* 370

\*011\* 41

\*012\* DNA

\*013\* Artificial Sequence

\*020\*

\*023\* Synthetic oligonucleotide probe

\*400\* 370

gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

\*010\* 371

\*011\* 1150

\*012\* DNA

\*013\* Homo sapiens

\*400\* 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggetggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgcggggcc gggactggcg ccgagggggc 200  
 tggggcggaa ggtcagagag ggagggcctg tggcacggcg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagtg ccaacttcgc gaagcggggc 300  
 tcactgctct ggaaccagca ggatggtaac ttgtccctgt cacagcgcca 350  
 gctcagcgag gaggagcggg gcgcactccg ggatgtggca gccctgaatg 400  
 gctctgaccc ggtccggatc ccaagcgac ccggggccct ggatggcctg 450  
 caagctggcg gctatgtctc ctcttttgc cctggctgct cctgggtgga 500  
 gtgcacctg tgggaccagc tgacctgca cgtggatgtg gccggcaacg 550  
 tggcggcggt gtgggtggcg acccaccgc ggggctgcgc gggccatgag 600  
 gtggaaggag tggacctgga gctgttcaac acctcggtgc agctgcagcc 650  
 gccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgctgg 700  
 agatggaaca ggcacagaag gccagaacc cccaggagca gaagtccctc 750  
 ttgcacaaat actggatgta cctcattccc gtggtcctgt tctcctgat 800  
 gtcaggagca ccagacacc ggggcacggg tggggcggg ggtgggggtg 850  
 gtggtggggg tagtggcctt tctgtgtgc caccctccct gtaagtctat 900  
 ttaaaacat cgaagataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttcacgc agccaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatactta ttcagaaacc 1050  
 caagggaatgg ctgtcccat cctcctgtgg ctgtgtggag ctgagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu			
				35					40					45			
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe			
				50					55					60			
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu			
				65					70					75			
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu			
				80					85					90			
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn			
				95					100					105			
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp			
				110					115					120			
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys			
				125					130					135			
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val			
				140					145					150			
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro			
				155					160					165			
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu			
				17					175					180			
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly			
				185					190					195			
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala			
				200					205					210			
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys			
				215					220					225			
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser			
				230					235					240			
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly			
				245					250					255			
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu				
				260					265								

00100 373

00110 1706

00120 DNA

00130 Homo sapiens

0000 373

ggagcgcgtgc tggaaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgccccc cagaccgggg 100

cagcaggtcg tcggggggcc caccatgctg gtgaactgct accttgcttt 150  
 tgtaggcttc ctggcctcct ggcctggggt ggaactgtca agatgcggg 200  
 ctaaaacccc tgggaaggcc tgcagcaatc cctccttcct tcggtttcaa 250  
 ctggactttc atcaggtcta cttcctggcc ctggcagctg attggttca 300  
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
 aaattgcat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
 ctagtggcct cctccttgtt ggattggctg ggtcgcaaga attcttgtgt 450  
 cctctttctc ctgaacttact cactatgttg cttaacccaa ctctctcaag 500  
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
 ctctctttct cagccttcga ggcttggtat atccatgagc acgtggaaag 600  
 gcatgaactc cctgctgagt ggatccagc tacctttgct cagctgct 650  
 ctctggaaca tgtgctggct gtagtggcag gctgggcagc tgaggctgta 700  
 gccagctgga tagggctggg gctgtagcg ccttttgttg ctgccatccc 750  
 tctcctggct ctggcagggg ccttggccct tcgaaacttg ggggagaaat 800  
 atjacgggca gctgctcttc tcaaggacct gtctggagg cctgcctg 850  
 ctctgttggg accgcgggt gctgctgctg ggcacatc aagctctatt 900  
 tgagagtgtc atcttcctct ttgtcttctc ctggacacct gctgtggacc 950  
 cacacggggc cctctgggc attatctctc ccagcttcct gccagccagc 1000  
 ctgtttggct cttcctgtta cgttatcgcc acctccaaga ggtaccaact 1050  
 tcagcccatg cactgctgt ccttgcctgt gctcctctc gtctctctc 1100  
 tcttcctgtt gactttctct accagccag gccaggagag tcgggtggag 1150  
 tccttcctag cctttctact tattgagttg gctgtggat tatacttct 1200  
 cagcatgagc ttcctacgga gaaaggctat cctcgagaca gagcaggctg 1250  
 gtgtactcaa ctggttcagg gtacctctgc actcactggc ttgcctaggg 1300  
 ctctctgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatggt 1350  
 cagcatttgc tctgctgtca tgggtgatggc tctgctggca gtggtgggac 1400  
 tcttcacctg gtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
 gaggagccct atgcctctga gctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgaacttt gtgactgtcc tgtgggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaaggtag caaaagttcc 1650  
 ctctgtgtta ctccattta gaaaataaac acttttaaat gatcaaaaaa 1700  
 aaaaaa 1706

(210): 374  
 (211): 450  
 (212): PET  
 (213): Homo sapiens

(409): 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

(210) 375

(211) 1093

(212) DNA

(213) Homo sapiens

(400) 375

gcgacgcgcg gcggggcgcg gagaggaaac gcggcgcgcg gccgggcccg 50

gccctggaga tggccccgg cgcgcggggc tgggtgttgtc tegtgtctctg 100  
 gctccccggc tgcgtcggcg cccacggcctt ccgtatccat gattatttgt 150  
 accttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 ccgtgccaagg accttggttg tatctttcac acaaggctatg agcagattca 250  
 actgtccccc gctgaacctc cagaggcctg cgggggaactc agcaacgggt 300  
 tcttcaccca ggaccagatt gctctgttggt agaggggggg ctgctccttc 350  
 ctctccaaga ctgggttggt ccaggagcac ggcgggcggt cgtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctactggag atgatccagg 450  
 acagtaacca ggcacagct gacatccccg cctcttctct gctgggcaga 500  
 gacggctaca tgatccggcg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600  
 tgcacccggc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgaat ctgagctggg aaggggaaac ccaggaattt tgcacttgg 700  
 natttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
 tttgggggtt gctaggtga aaggggaagc acaccactgg ccttccttc 800  
 cccagggccc ccaaggggtg ctcatgctac aagaagaggg aagagacagg 850  
 cccaggggtt tctgggtaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcttgagagg catctgtgac ctgtcacact cactgggtc cagcctccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10						15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40						45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr		
	50	60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly		
	65	75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val		
	80	90
Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln		
	95	105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp		
	110	120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg		
	125	135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr		
	140	150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile		
	155	165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu		
	170	180
Leu Gln Pro Pro Trp Thr Phe Trp		
	185	

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
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 ggcctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggccaagca agtgactggg aaaatgccca tctctctcta 150  
 ctggccttac ggctgtcact gccgactagg tggcagaggc caacccaaag 200  
 atgccaaggga ctggtgtgtc cagaccatg actgctgcta tgaccacctg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400



aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 495

<210> 378

<211> 116

<212> PPT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val  
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys  
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly  
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr  
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys  
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile  
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe  
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu  
110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

caagagagtg gatgttcccc tggg 24

<210> 381

<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 381  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382  
 <211> 764  
 <212> DNA  
 <213> Homo sapiens

<400> 382  
 ctgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50  
 gggcatgtgg aggggtgccc gcaacaaccag acgcccagtc acaggcgaga 100  
 gacctgggat gcaaccggcca gaggccatgc tgcctgtgtc cacgcttgcc 150  
 cctctggggg gcccacactg ggcagggaaag atgtatggcc ctggaggagg 200  
 caagtatttc agcaccactg aagactaaga ccattgaaat acagggctgc 250  
 ggtgtctgt aggtctcttc ctggtgaaaa gtgtccaggt gaaaattgga 300  
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
 caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
 ctctctcccg gggatgtg atgtacacca gcaaggacgg ctattcttat 450  
 ttggggaagc ttgatggcca gatctctctt gctaccacca gccaaagagg 500  
 gagggtgtg gtgggcctct atggccagta tcaactcctt ggcattcaaga 550  
 gatttggctt tgaatggaa tatccactag aggagccgac cactgagcca 600  
 ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650  
 ggtatggggc catccagact gaggccatct gtgtggtggt ggtgatggt 700  
 actggagtaa ctgagtggg acgtgaatc tgaatccacc aataaataaa 750  
 gcttctgcag aaaa 764

<210> 383  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<400> 383  
 Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
 1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly  
                     20                    35                    50  
 Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr  
                     35                    50                    65  
 Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln  
                     50                    65                    80  
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly  
                     65                    80                    95  
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr  
                     80                    95                    110  
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met  
                     95                    110                    125  
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly  
                     110                    125                    140  
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val  
                     125                    140                    155  
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly  
                     140                    155                    170  
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro  
                     155                    170                    185  
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg  
                     170                    185

<210> 314  
 <211> 2179  
 <212> DNA  
 <213> Homo sapiens

<400> 314  
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 agctctgtgg ctgaactggg tgcctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggagctcag gtagccccaa attgcttjga agaatacatc 150  
 atgttttttg atangaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca ccccccacaa aaactgtaaa gatgcacaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgcg ggaatgcgg 300  
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(210): 335  
 (211): 513  
 (212): PRT  
 (213): Homo sapiens

(400): 385  
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 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg	155	160	165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys	170	175	180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser	185	190	195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu	200	205	210
His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe	215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys	230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu	245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly	260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu	275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser	290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu	305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe	320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu	335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile	350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu	365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu	380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly	395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile	410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu	425	430	435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
 440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
 455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
 470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
 500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 387

ggtcccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 388

gctgagatta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttgggtgt 150  
 ctoggacctc ccattgggaag aagatgaaat gtgtgtaaat tataatgacc 200  
 aacacccctaa tggctgggtat atctggatcc tctgtgtgtt ggttttgggtg 250  
 gcagctcttc tctgtggagc tgtggctctc tgcctccagt gctgggtgag 300  
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 caacctgatt ttagggtgtg attatcaatt taaagtatta acgacatctg 550  
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 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
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 agatagtatt tgaatgaagg tgaggggaga gtagaggaaa aagaaaagtt 1000  
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 tgtagataga aggtgaagga gattgctgaa gatataagc acatataatg 1150  
 ccaaacaggc gagaaaagaa aatttccctt ttacagtaa tgaatgtggc 1200  
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250  
 cagcatcatg ctaagaacct tggcatagg tatctgttcc catgaggact 1300  
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<210> 390  
 <211> 146  
 <212> PPT  
 <213> Homo sapiens

<400> 390  
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 Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp  
 20 25 30  
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
 35 40 45  
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu  
 50 55 60  
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
 65 70 75  
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
 80 85 90  
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
 95 100 105  
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
 110 115 120  
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
 125 130 135  
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
 140 145

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 391  
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<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 293

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 343

ccagtttggtg ctctcggacc taacatgcga agaagatgaa atgtgtg 47

<210> 334

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 334

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<210> 395

<211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 396  
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                   20                  25                  30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
                   35                  40                  45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
                   50                  55                  60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
                   65                  70                  75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
                   80                  85                  90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
                   95                  100                 105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
                  110                 115                 120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
                  125                 130                 135  
 Ser Gly Ser Ile Arg  
                  140

<210> 396  
 <211> 1639  
 <212> DNA  
 <213> Homo sapiens

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<010> 397

<011> 353

<012> PRT

<013> Homo sapiens

<000> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30

Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45

Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60

Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75

Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe Ser	105	106	105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly Leu	110	115	120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser Asp	125	130	135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser Ala	140	145	150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu		350		

<C10> 398

<C11> 23

<C12> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctggccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

gggttggtgcc cgaaaggctc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

aaacccaag cttactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga agggtagact acgttggctt totggaaggg 100

gaggctatat gogtcaattc cccaaaacaa gttttgacat ttcccttgaa 150

atctcattct ctattatttc actgcaagtg cctgctgttc caggccttac 200

ctgctgaggc ctaacggggg agccaggatg gggacagaat aaaggagcca 250

cgactcttgc caccactcg cactcagaact ctgaactcag acctgaaatc 300

ctctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

cttcagacct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctggttttta ctctctatgg actccttcca ctggactgaa gacaactaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550



gaatcttaag gaggaactgag tctttgcaag acacaaagcc tgcgaatoga 600  
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 aaactaccag acccctgaac attatactct ccggaagatc agcagcctcg 700  
 ccaattcttt tottaaccatc aagaaggaac tccggtctct tcatgccac 750  
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 gggaactaga cattctttctg caatggatgg aggagacaga ataggaggaa 900  
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
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 attttgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150  
 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200  
 ctttaaaaaa attcacagat tatatttata acctgaactag agcaggtgat 1250  
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 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgac acctacctta caattactga 1450  
 ccacccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatccctaac gccacgcatg tatttctaca aataaagttt tctttgcata 1550  
 ccacacacac aaaaaaaaaa a 1571

<110> 402

<111> 261

<112> PRT

<113> Homo sapiens

<400> 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25					30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40					45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

(210) 403

(211) 28

(212) DNA

(213) Artificial Sequence

(220)

(225) Synthetic oligonucleotide probe

(400) 403

ctctgtgtgt ctccagattt caggccta 28

(210) 404  
 (211) 26  
 (212) DNA  
 (213) Artificial Sequence

(220)  
 (221) Synthetic oligonucleotide probe

(400) 404  
 agtctctctt aagattctga tgtcaa 26

(210) 405  
 (211) 238  
 (212) DNA  
 (213) Homo sapiens

(400) 405  
 ccgttatcgt cttgcgtac tgtgaatgt ccgtcccgga ggaggaggag 50  
 aggtttttgc cgtgaccca gagatggccc cgagcgagca aattcctact 100  
 gtccgggtgc ggggtaccc tggccgagct agcaaccttt cccctggatc 150  
 ccacaaacac tgcactccaa atgcaaggag aagcagctct tgcctgggtg 200  
 ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
 cctagggtac attgaagagg aaggtcttct aaagctttgg caaggagtga 300  
 caccggccat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350  
 tatgaacatc tccgagaggt tgtgttttgg aaaagtgaag atgagcatta 400  
 tcccccttgg aaatcagtca ttggagggat gatggctggg gttattggcc 450  
 agttttttag caatccaaat gacctagtga aggttcagat gcaaatggaa 500  
 ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
 tgcatttgca aaaatcttag ctgaaggagg aatacagggg ctttgggcag 600  
 gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
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 ggacaatata atgactcacg gtttatcaag tttatgttct ggactggtag 750  
 cttctattct gggaaacacca gccgatgtca tcaaaagcag aataatgaat 800  
 caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
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 cttacttatg aaaaaatcag agagatgagt ggagtcagtc catttttaa 998

<110> 406  
 <111> 323  
 <112> PFT  
 <113> Homo sapiens

<400> 406

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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Gln	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr	
	260 265 270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly	
	275 280 285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met	
	290 295 300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg	
	305 310 315
Glu Met Ser Gly Val Ser Pro Phe	
	320

(210) 407

(211) 31

(212) LNA

(213) Artificial Sequence

(320)

(321) Synthetic oligonucleotide probe

(400) 407

gggggatccc gttatgtgtt tgcgtacttg c 31

(210) 408

(211) 34

(212) DNA

(213) Artificial Sequence

(320)

(321) Synthetic oligonucleotide probe

(400) 408

gggaaattct taaaatggac tgactccact catc 34

(210) 409

(211) 1467

(212) DNA

(213) Homo sapiens

(400) 409

gggacgggtg ggggggggac gggggcaggg ttgtggggca gcagtctcct 50

tcctgggggc gggcctgaag tcggcgtggg cgtttjagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

cagataattt tcgttggcca gaatgtgaat gtattgactg gattgagaga 200

agaaatgctg tggcatctgt tgtgcaggt atattgttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tccaaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400  
 ctgttttagga agaacagggtg ctcgagtttg gcttttcaat ggtttcatgt 450  
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatt 500  
 gtaacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550  
 tgcacttata ttttttagca ctctgatcta caaatttggga agaaccgaag 600  
 agctatgyac ctgagatcac ttcttaagtc acattttctt ttgtttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaatggag 700  
 tagattgtac attaatgttt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttatct ttcattgcct agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
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 gctcatgctt gtaatccag cacttttggga ggcgaggcg ggcgattgc 1000  
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
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 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcaatgagc 1300  
 cataaaaggt tttcagcaag ttgtaactta ttttggcta aaaatgaggt 1350  
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<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20				25					30	

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
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<210> 411

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

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<210> 412

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

(1400) 413

atggcaggct tcttagataa ttttcgttgg ccagaatgtg 40

(1210) 414

(1211) 1337

(1212) DNA

(1213) Homo sapiens

(1400) 414

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gcagctgggc cactggcggc ccgcaaacct ccgtctcacc ctctggggcc 100

actgcctcta gaggaggggc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg cctctctcat cgaagcaggg 250

aagtgggagc ctgagccct cgggtggaa gctgacccaa gccacccctc 300

acctggacag gatgagagtg tcaggtgtgc ttgacctct ggccctcctc 350

tttgccatag tcaagacatg gatgtttatt cgaagctaca tgagcttcag 400

cctgaaaaac atccgtctgc cactgtggct ggcagcctcg ccacccaagg 450

agatccaggt taaaaagtac aagtgtgggc tcatcaagcc ctgcccagcc 500

aactactttg cgtttaaaat ctgcagtggg gcgcaccaag tctggggccc 550

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ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaattc cgggggggtgc actggctgtg gctggcctct 750

acgacgctcc agggacccaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttctctacg aaaaacaactg ggcttcgggg acagctgggt 850

cttcctatgga gccaaaagacc tcaggggtta aagccctttt gagcagttct 900

taaagaacag ccacagacaca aacaaatag agggatggcc agagctgtgt 950

gagatggagg gctgcctgcc ccggaagcca ttttaggggtg gctgtggctc 1000

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gcaggtcctt gcaogctgtg tcgcgcctct cctctctgga aacagaaacc 1150

tccacagca cactctacc ggaagaccag cctcagaggg tcttcttgga 1200



accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250

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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 124

<212> PRT

<213> Homo sapiens

<400> 415

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Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
20 25 30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
35 40 45

Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
50 55 60

Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
65 70 75

Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
80 85 90

Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
95 100 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
110 115 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
125 130 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
140 145 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
155 160 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
170 175 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
185 190 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
200 205 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
215 220

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 416  
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<210> 417  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
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<210> 418  
<211> 16  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
taattctaaag tgtgacctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 419  
tcctgactcct aagtcaggca ggag 24

<210> 420  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 420  
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<210> 421

\*2118 46  
 \*2120 DNA  
 \*2130 Artificial Sequence

\*2200  
 \*2230 Synthetic oligonucleotide probe

\*2400 471  
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\*2500 482  
 \*2510 1701  
 \*2520 DNA  
 \*2530 Homo sapiens

\*2200  
 \*2210 unsure  
 \*2220 1528  
 \*2230 unknown base

\*2400 412  
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 ggcctcttaa ttgaggtggg ttagactaag aatatagctt atgaacacat 800  
 ttctgagtcac ttgcattgaag tcaggcataa agatcagaag acctcagtgc 850  
 ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgtacaatg gctcgtcac aactccccct tctaccaga gtgtgtctg 950  
 gacagttttt tatagaaggc cccagatttc aatggaacag ctggaaaagc 1000  
 ttcaggggac attgtttctc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gctctcaat cagcccatgg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
 gtgtaggaat cttggttggc tgtctctgac tctctctggc tgtttatttc 1200  
 attgctagaa agattcggaa gaagaggctg gaaacccgaa agagtgtggt 1250  
 cttcactca gcacaagcca cgaactgagg ataacttctt tctcagatac 1300  
 catggatgtg gatgacttc cttcatgctt atcagggaag ctctaaaatg 1350  
 ggggtgtagga tctggccaga aacactgtag gatttgtaag cagatgtctt 1400  
 ccttcctctg gacatctctt agagaggaat ggaaccaggc tctcattcca 1450  
 ggaagaactg cagagcttcc agcctctcca aacatgtagg aggaaatgag 1500  
 gaaatcctg tgttgtaat gcagagacca aactctgttt agttgcaggc 1550  
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
 tttcctaga tatactggg gatctctctt taggataaag agttgtgtt 1650  
 gaattgtat attttgata aatatatttg gaaactaaag tttctgactt 1700

1 01

0210 - 423  
 0211 - 337  
 0212 - PRT  
 0213 - Homo sapiens

0400 - 423  
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
 1 5 10 15  
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
 20 25 30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly		
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His		
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala		
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu		
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His		
170	175	180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro		
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe		
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val		
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln		
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Phe		
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn		
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr		
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly		
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile		
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser		
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<010> 424

<011> 18

<012> DNA

<013> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 414  
gtaaagtcgc tggccagc 18

<210> 415  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 415  
cccgatctgc ctgctgta 18

<210> 416  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 426  
ctccactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 427  
cagaaaccca tgatacccta ctgaacaccg aatcccttg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
acattttgoc tcttggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tgggtcatta ccacagctca 150  
aactgtgttt gggactccct ccacaaaaac tggctccgga tcagggaaca 200  
ctaccaaaac aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtaccacaga cccacccatt gaccctggga 350  
 ggggttgatg tacaacagca actgcaccca catgtgttac caatttttgt 400  
 cacacacctt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagctcctac atccattcct tgttcccgga aggcctcctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gctcctcaac tccagtggc acagatgag actttgcagt gaaccacccct 650  
 gcaggcctcc aaaggagcac acatgccctc gaggaagcca ccacagaatc 700  
 agcaaaggga attcagtaag ctgtttcaaa ttttttcaac taagctgctt 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttaact 850  
 caaaatattc ttgaaatttc agaaaatatg ttctatgtag agaattccaa 900  
 ctttttaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgtctgct ggatgatag catattaaaa catatttggg aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

0210: 429

0211: 209

0212: PRT

0213: Homo sapiens

0400: 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5				10						15

Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20					25						30

Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35					40						45

Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50					55						60

Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65					70						75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
			80					85						90

Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
	110	115	120
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly			
	125	130	135
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp			
	140	145	150
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln			
	155	160	165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp			
	170	175	180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His			
	185	190	195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln			
	200	205	

(210) 430  
 (211) 1257  
 (212) DNA  
 (213) Homo Sapien

(400) 430  
 ggagagagggc gcgcggggtga aaggcgccatt gatgagccct ggcggggccct 50  
 gggagcgagg cggagccaga cgcctgaccac gttccctctcc tcggctctct 100  
 ccgcctccag ctccggggtg ccgggcagcc gggaagccatg ccaccccagg 150  
 gccccgcgcg ctcccccag cggctccggcg gcctccctgt gctccctgctg 200  
 ctgcagctgc ccgggcgcgc gagcgcctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggccaga gggaggtggt ggaacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggct gagacgggag ccctggggcc 350  
 aatgtttatc cgggtacacc tgggacccca ggtcgggatg gattcaaagg 400  
 agaaaaaggg gaatgtctga gggaaagctt tgagggtcc tggacccca 450  
 actacaagca gtgttcctgg agttcattga attatggcat agatcttggg 500  
 aaaattggcg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttgggctaaa atgcagaaat gcctgctgct 600  
 agcgttggtg ttccacatcc aatggagctg aatgttcagg acctcttccc 650  
 attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700



aattaatatt catogcaott cttctgtgga aggactttgt gaaggaattg 750  
ctgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcattattat 850  
tgaagaacta ccaaaaataaa tgctttaatt ttcatttgc acctotTTTT 900  
ttattatgcc ttggaatggt tcaottaaaat gacattttta ataatgttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaaat aaaaattatt 1250  
tcaaca 1257

010> 431  
011> 243  
012> PRT  
013> Homo Sapien

0400> 431  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 433

ggcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<230> 434

atgacgctcg tccaaggcca c 21

<210> 435  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 425  
ccacactgta ccaccatgt 19

<210> 436  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 436  
ctctccaggca ccactctgttc tccc 24

<210> 437  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 437  
caggc tggc attcaagtc 19

<210> 438  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 438  
tgacctggca aaggaagaa 19

<210> 439  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Synthetic oligonucleotide probe

<400> 439  
cagccacct ccagtcctaag g 21

<210> 440  
<211> 19

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 440  
 gggtcgtatt ttggagaga 19  
  
 <210> 441  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 441  
 ctggccctca gaggaccaat 20  
  
 <210> 442  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 442  
 tctctatcca ctctccctag ctcca 25  
  
 <210> 443  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 443  
 ctggcaggag ttaaagttcc aaga 24  
  
 <210> 444  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 444  
 aaaggacacc gggatgtg 18  
  
 <210> 445  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445  
agcgtagact ctctccaggc aaccag 26

<210> 446  
<211> 22  
<212> LNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 446  
caattctgga tgagggtgga ga 12

<210> 447  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 447  
caggaactgag cgcttggtta 20

<210> 448  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 448  
caaaagcgcca agtaccggac c 21

<210> 449  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 449  
ccagacctca gccaggaa 18

<210> 450  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccctagetga ccccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctyacaagc agttttotga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccacct cctttttcct ttgttt 26

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctggtgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 454

ccatgacctgc tcagccaaga a 21

<210> 455

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 455  
 cacgaaatct ggaaacctac agt 23

<210> 456  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 456  
 ccttgaaaag gacccagttt 20

<210> 457  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 457  
 atgagtcgca cctgctgttc cc 22

<210> 458  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 458  
 tagcagctgc ccttggtta 18

<210> 459  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 459  
 aacagcaggt gcgactcatt ta 22

<210> 460  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 460  
 tgctaggcga cgacacccag acc 23

<210> 461  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 461  
   tggacacgtg gcagtgga 18  
  
 <210> 462  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 462  
   tcatggtctc gtcccatc 19  
  
 <210> 463  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 463  
   caccattgt ttctctgtct ccccatc 27  
  
 <210> 464  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 464  
   caggcatcct tggagtag 18  
  
 <210> 465  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 465  
   tcccattag cacaggagta 20  
  
 <210> 466



<211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 466  
 aggcctcttgc ctgtcctgct gct 23  
  
 <210> 467  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 467  
 ggcacagagtc ccacttgt 18  
  
 <210> 468  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 468  
 actgctccgc ctactacga 19  
  
 <210> 469  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 469  
 aggcatactc gccgtcctca 20  
  
 <210> 470  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 470  
 aaggccaagg tgagtcacat 19  
  
 <210> 471  
 <211> 20  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

ccagtggtgtg cgaaacctaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcttc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaagccaaagg tgagtccat 19

<210> 474

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

tcaggtgga ccccaattca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

-220-

-223- Synthetic oligonucleotide probe

-240- 476

ggagagctta taggcccaat ctgg 24

-210- 477

-211- 50

-212- DNA

-213- Artificial Sequence

-220-

-223- Synthetic oligonucleotide probe

-240- 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

-230-

-1-